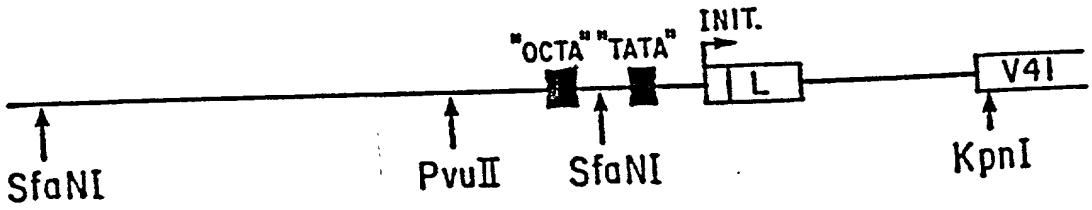


MOPC-41 κ CHAIN GENE

FIG. 1A

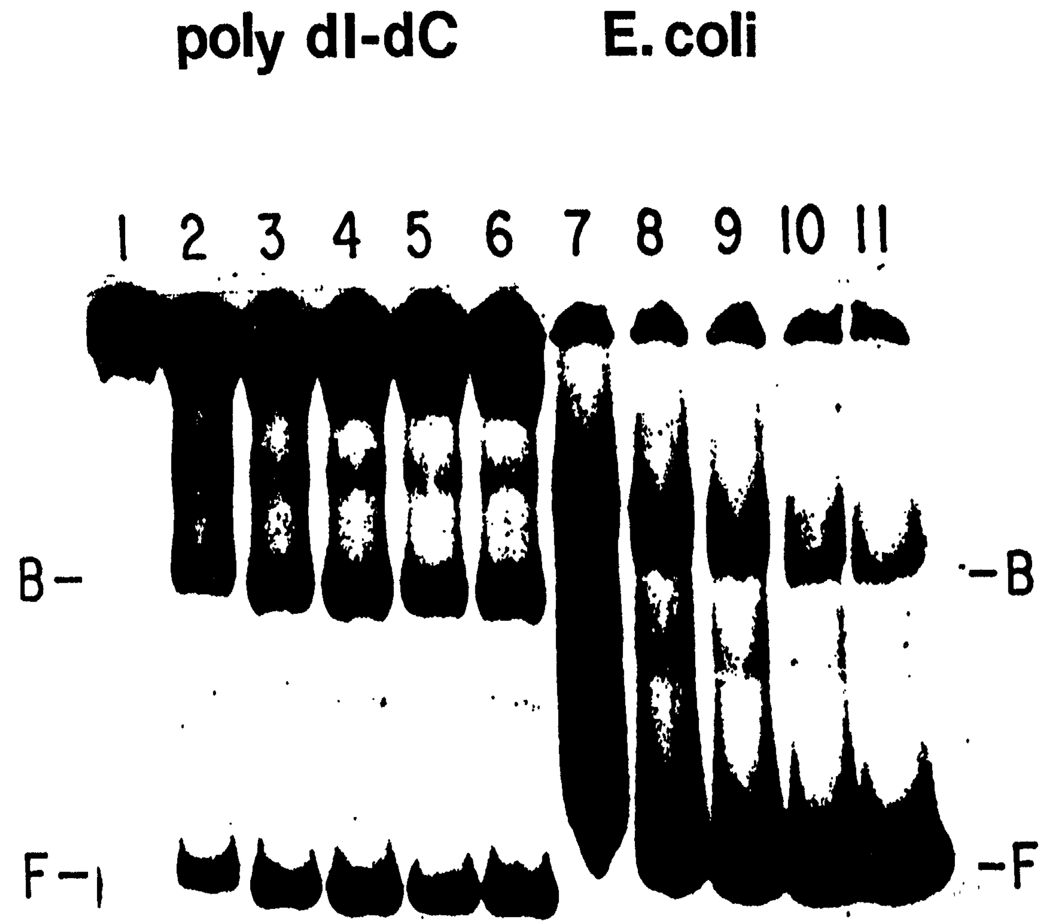


FIG.1B

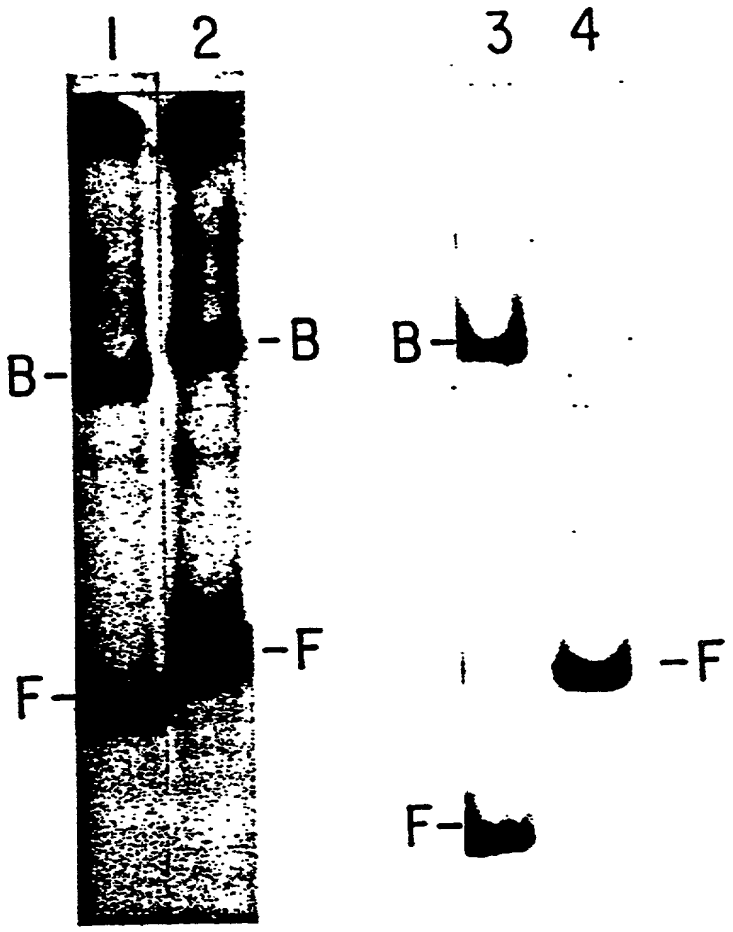


FIG.1C

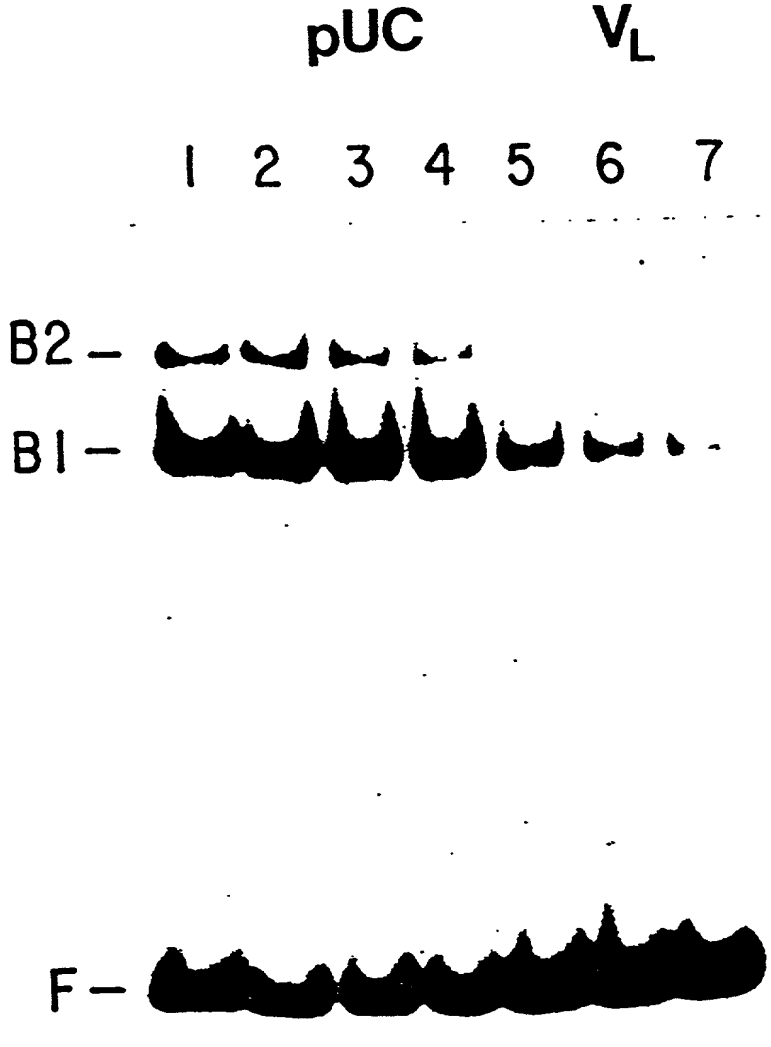


FIG.2A

FIG. 2B

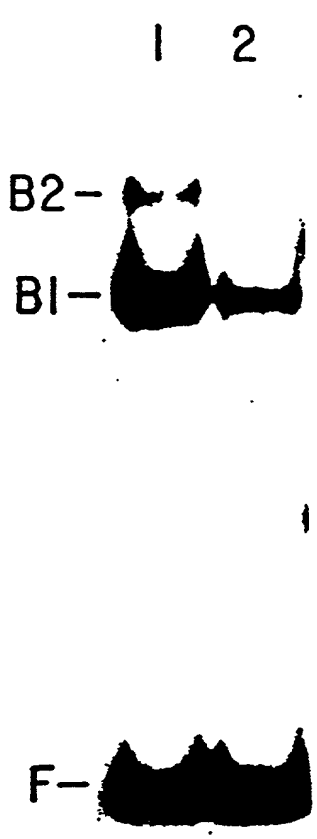
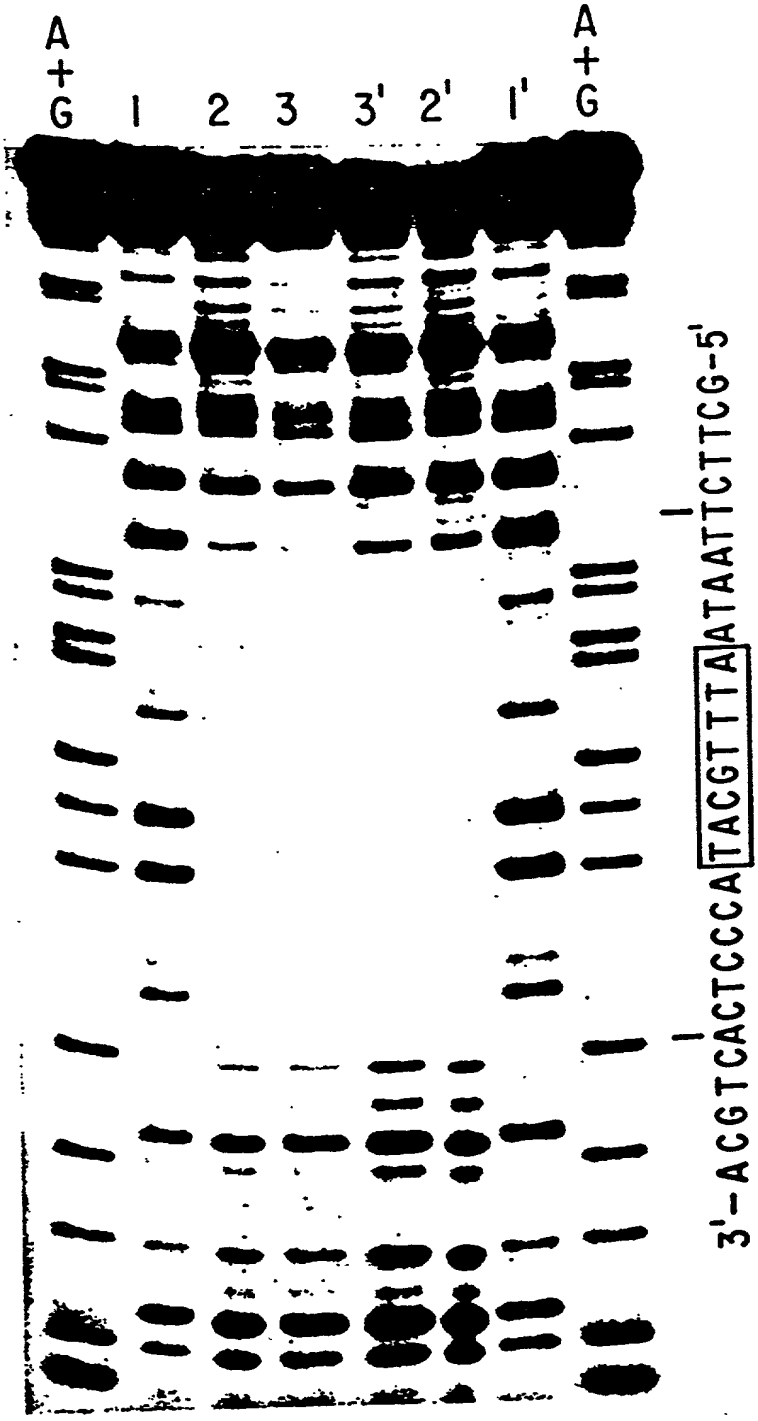


FIG.3



V_L coding strand (-66)	TCTTAATA*	ATTTGCAT	ACCCTCAC*
V_H non-coding strand (-50)	CGCACATG	ATTTGCAT	ACTCATGA
J_H-Cμ coding strand (166)	CCTGGGTA	ATTTGCAT	TTCTAAAA

FIG.4A

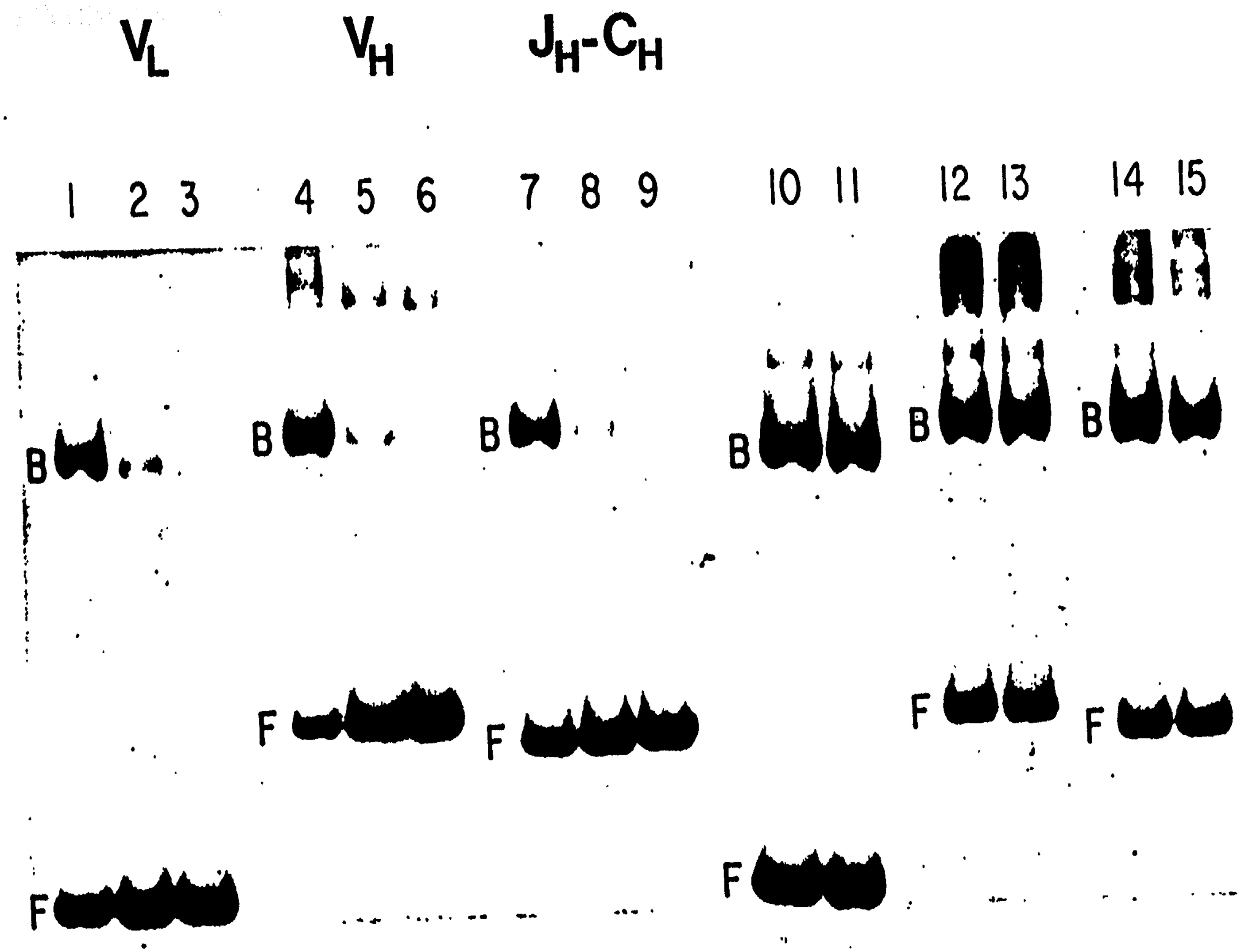


FIG.4B

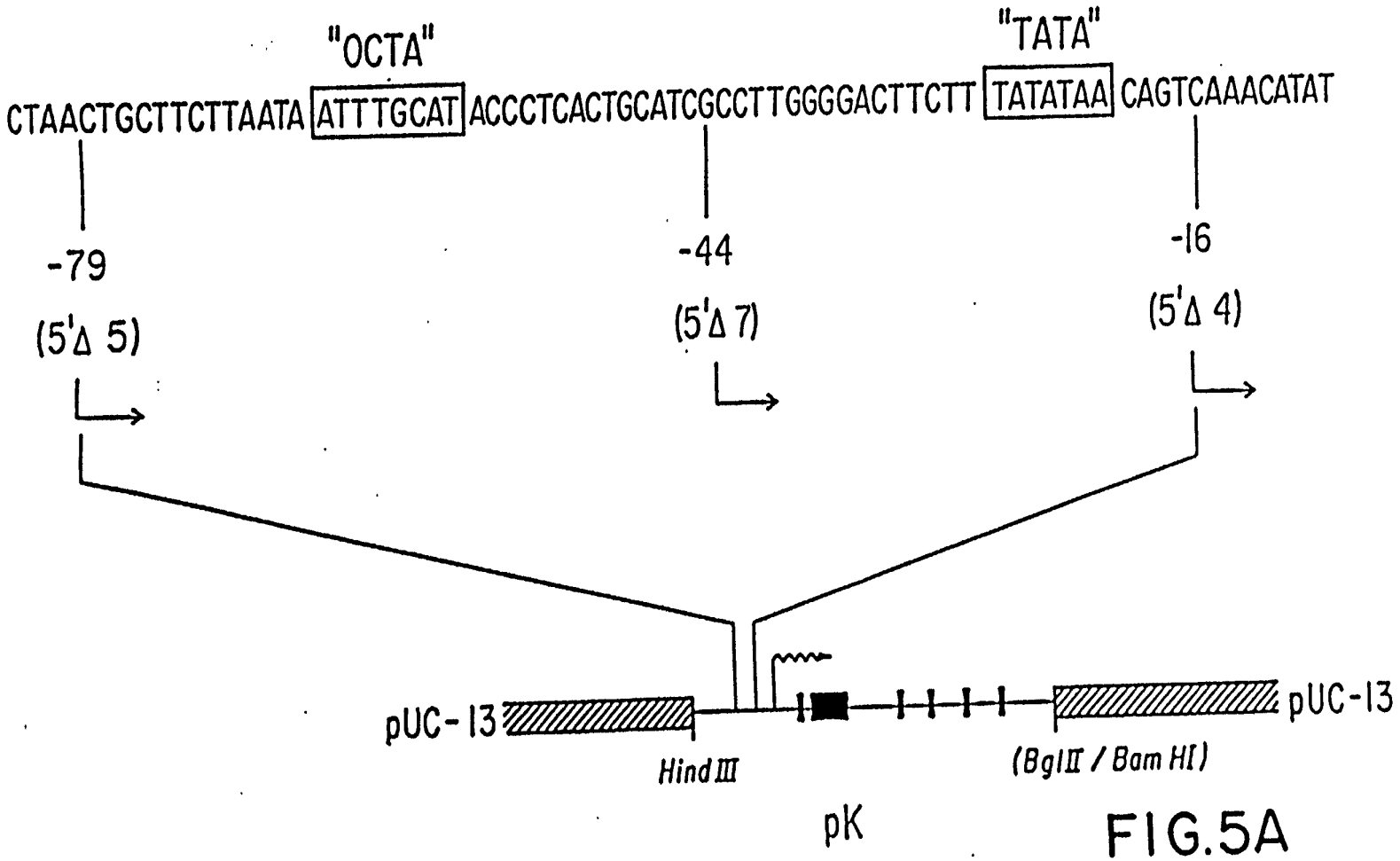

"OCTA"
"TATA"
CTAACTGCTTCTTAATA ATTTGCAT ACCCTCACTGCATCGCCTTGGGGACTTCTT TATATAA CAGTCAAACATAT
-79
(5'Δ 5)
-44
(5'Δ 7)
-16
(5'Δ 4)
pUC-13
pUC-13
Hind III
(BglII / Bam HI)
pK

FIG.5A

FIG.5B

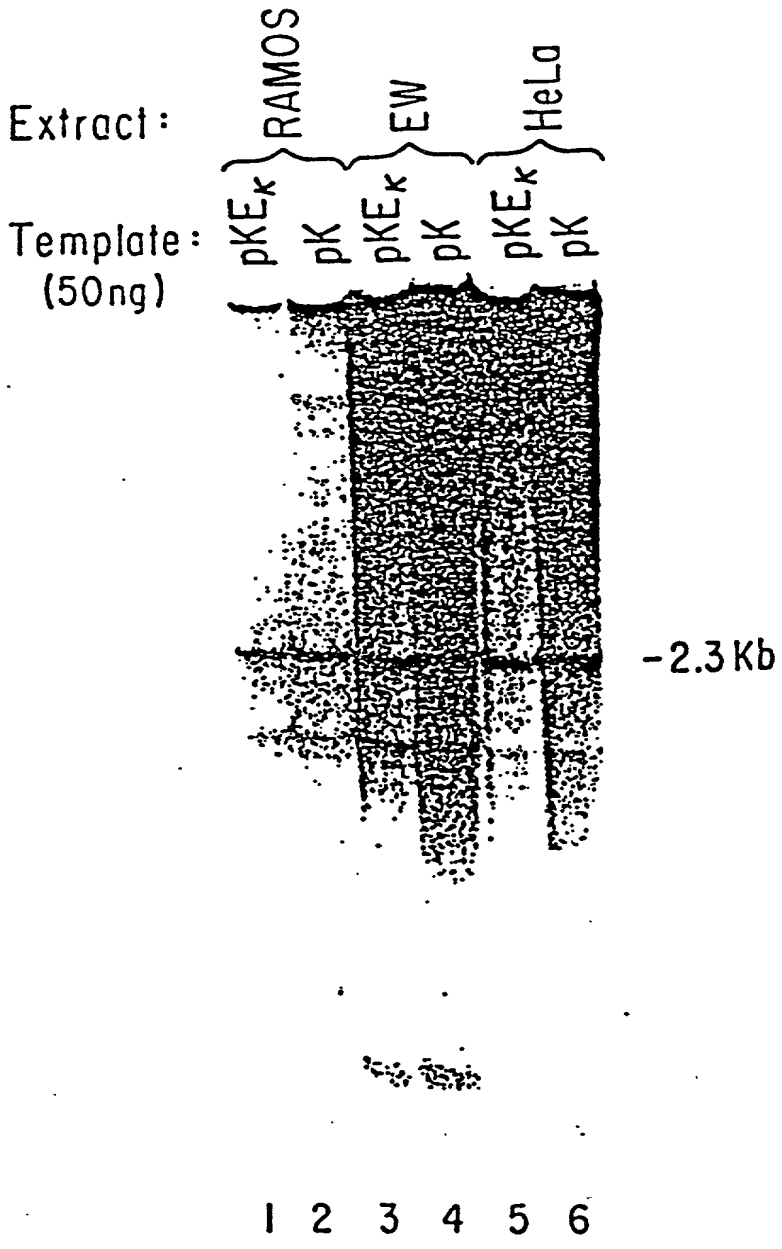

Extract:
RAMOS
EW
HeLa
Template:
(50ng)
pKEκ
pK
pKEκ
pK
pKEκ
pK
-2.3Kb
1 2 3 4 5 6

FIG.6

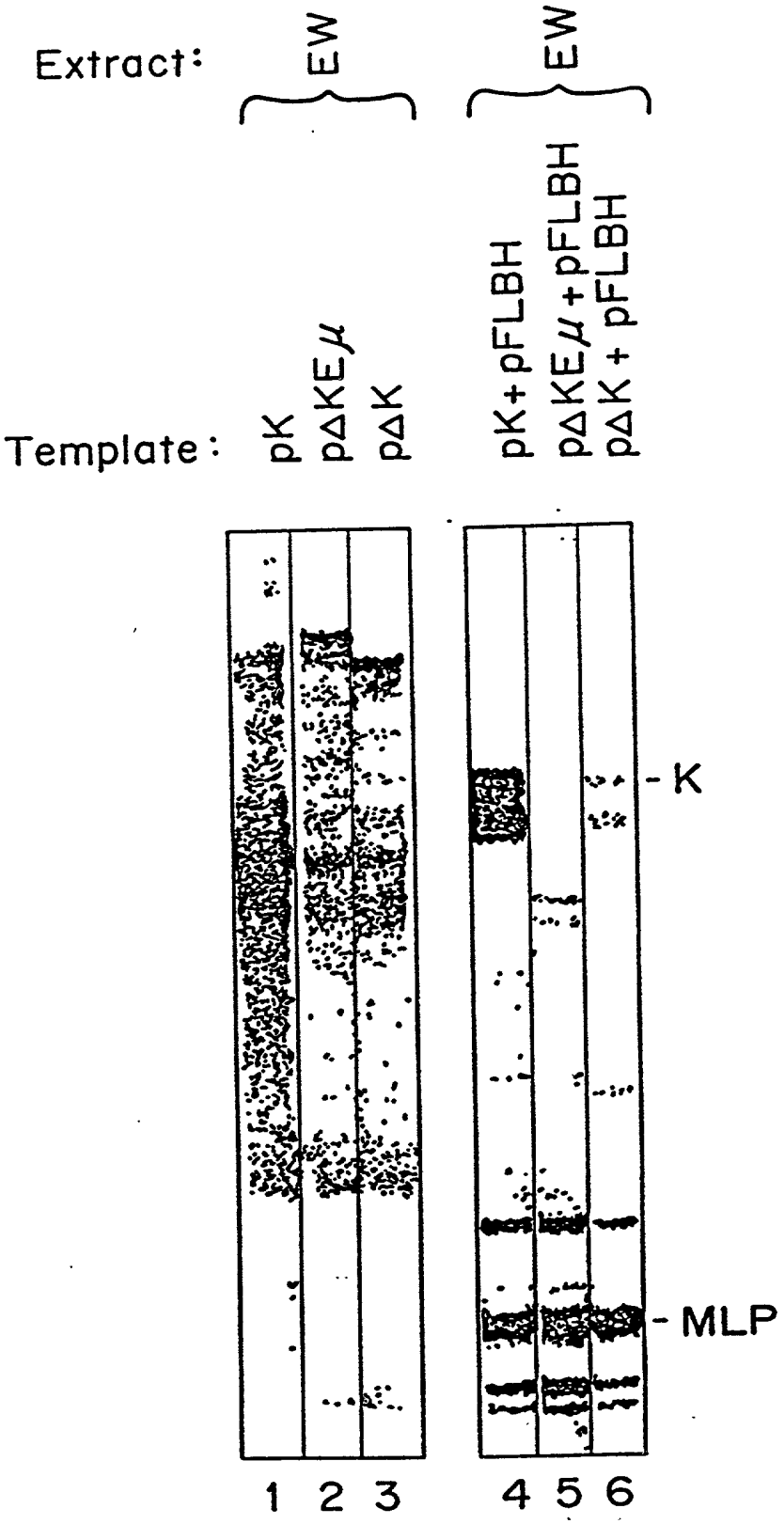
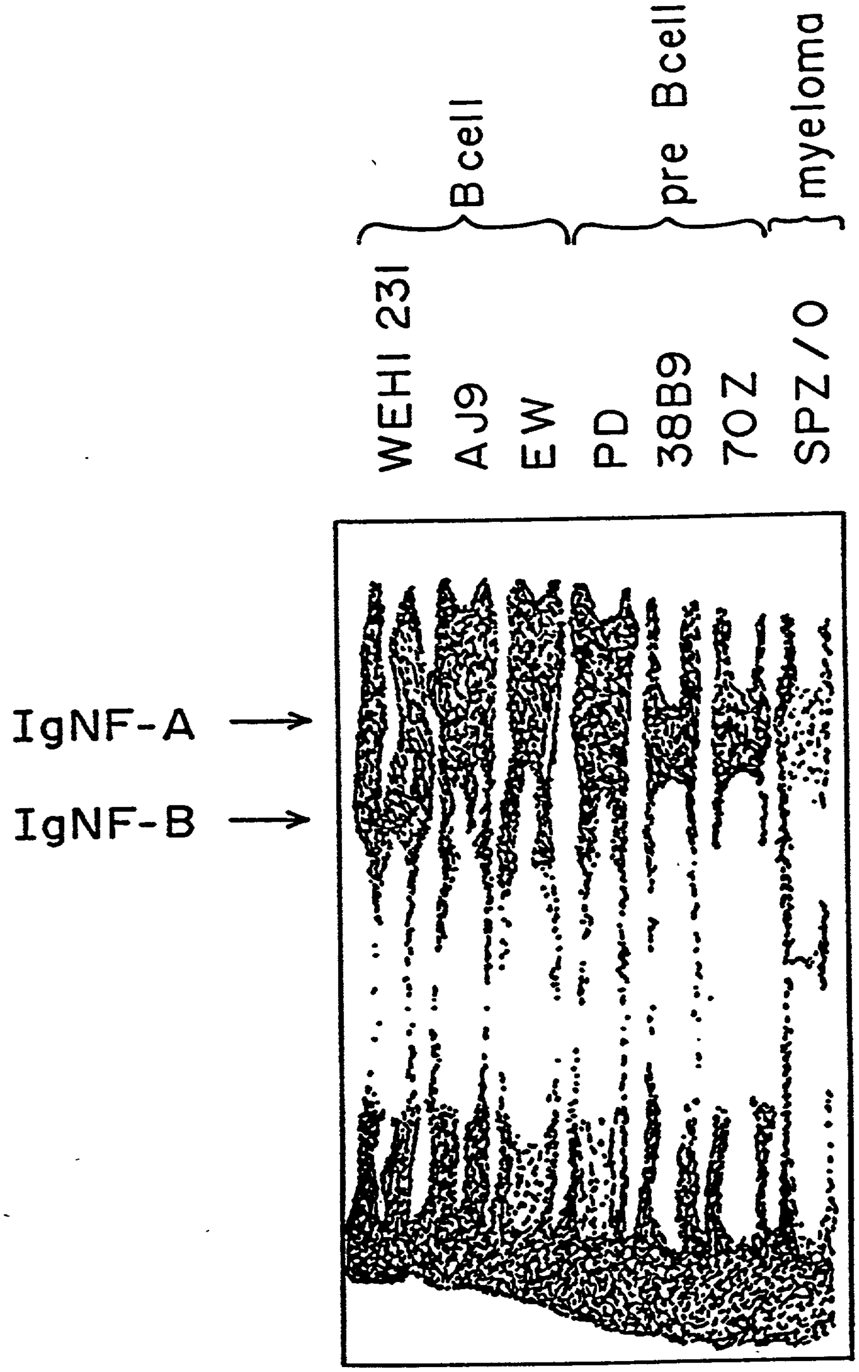
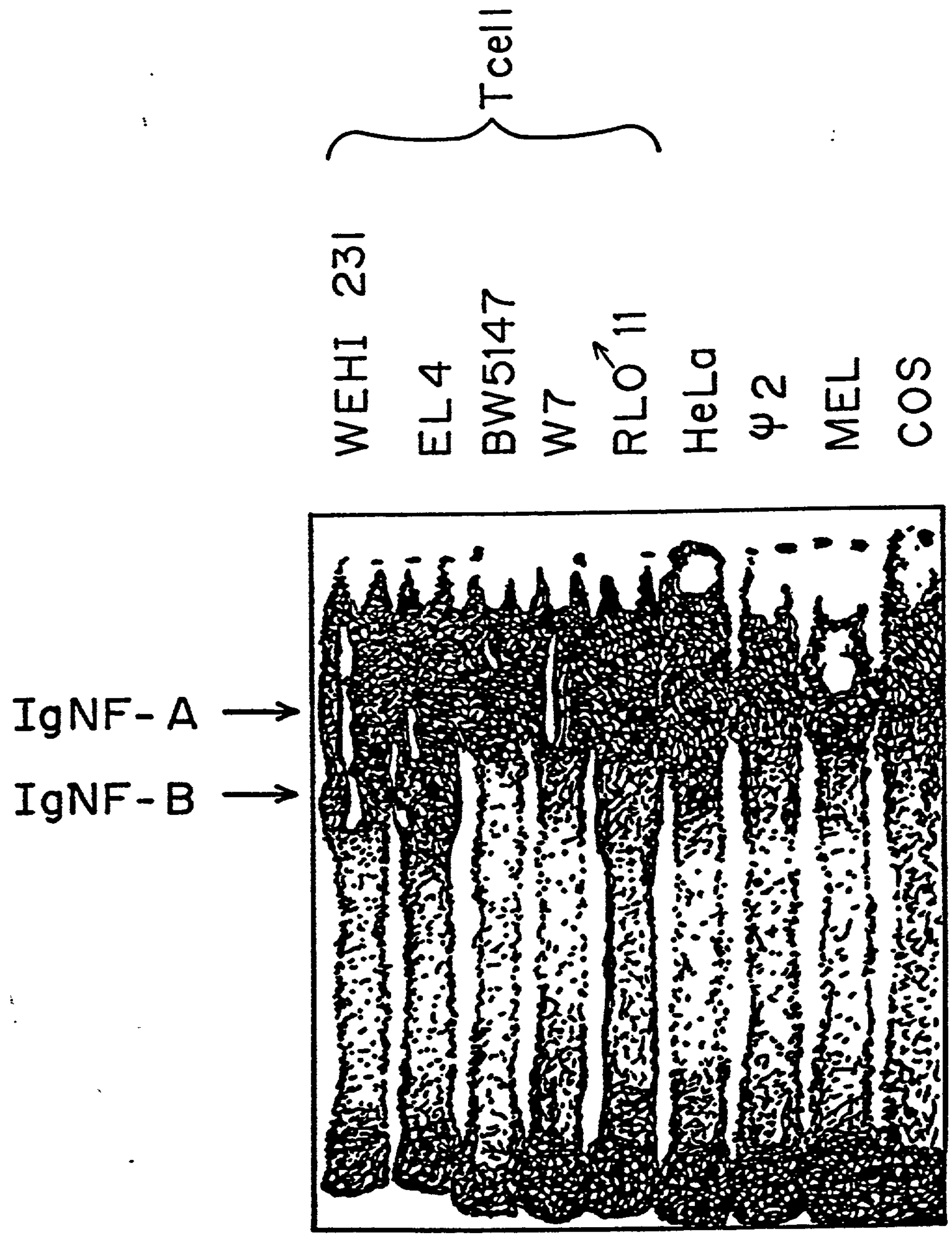

Extract:
EW
EW
Template:
pK
pΔKEμ
pΔK
pK+pFLBH
pΔKEμ+pFLBH
pΔK+pFLBH
-K
-MLP
1 2 3
4 5 6

FIG.7



WEHI 231
AJ9
EW
B cell
PD
38B9
70Z
pre Bcell
SPZ/0
myeloma
IgNF-A
IgNF-B

FIG.8



Tcell
WEHI 231
EL4
BW5147
W7
RLO 11
HeLa
ψ2
MEL
COS
IgNF-A
IgNF-B

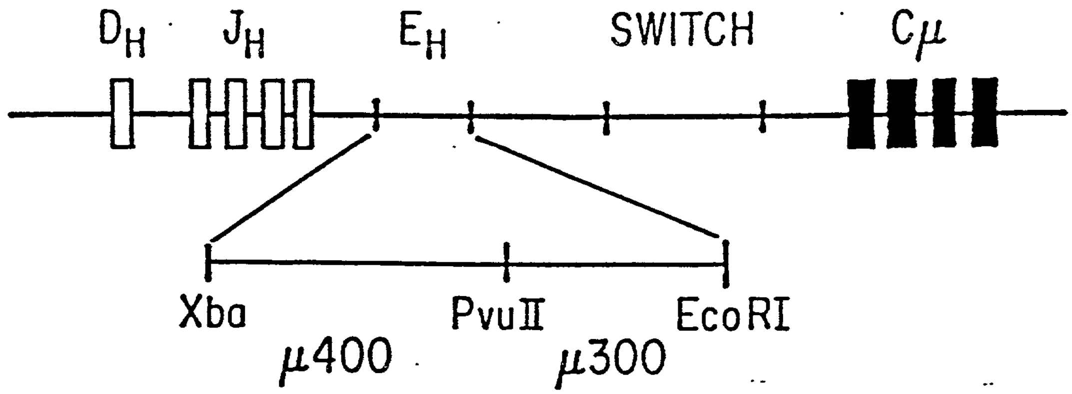

D_H
J_H
E_H
SWITCH
$C\mu$
Xba
PvuII
EcoRI
μ400
μ300

FIG.9A

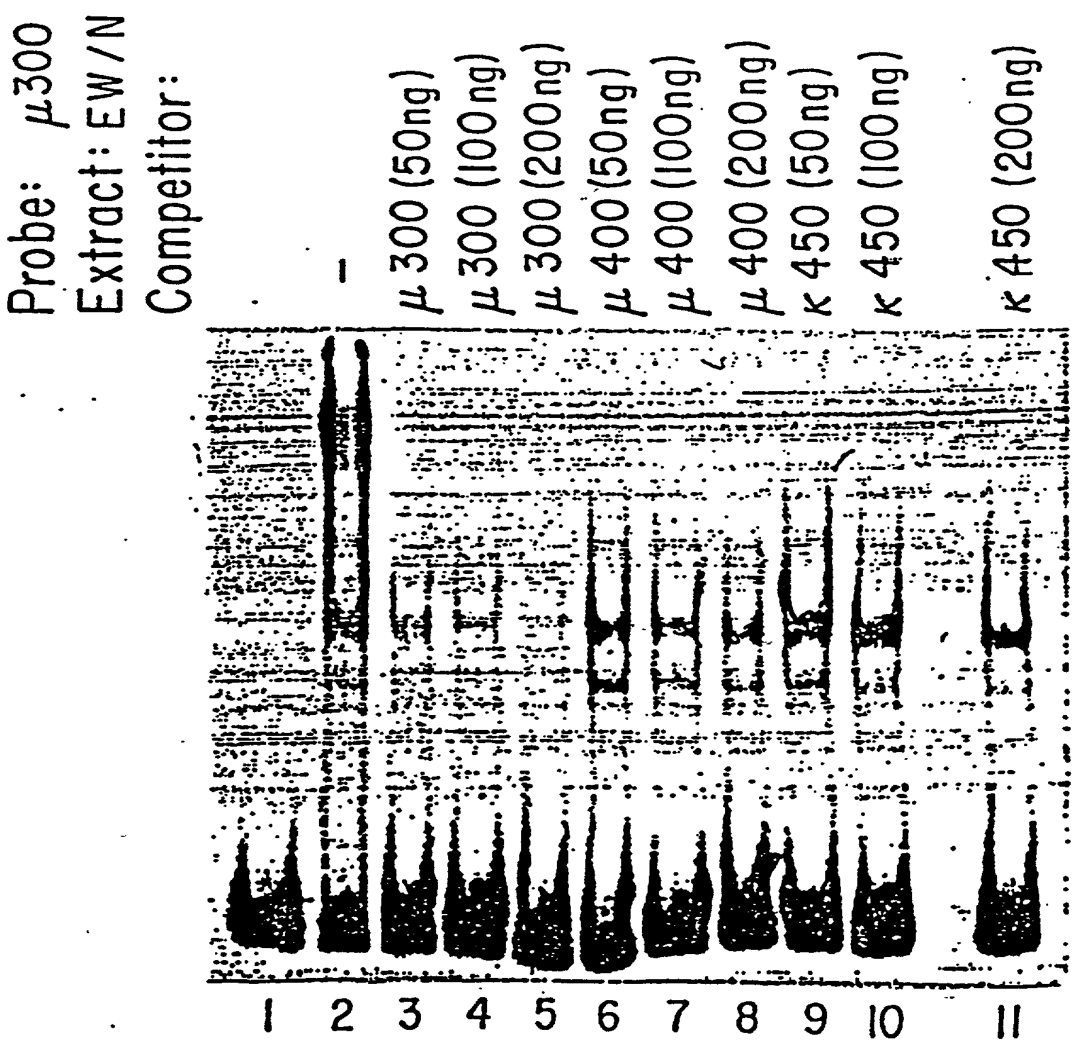

Probe: μ300
Extract: EW/N
Competitor:
-
μ 300 (50ng)
μ 300 (100ng)
μ 300 (200ng)
μ 400 (50ng)
μ 400 (100ng)
μ 400 (200ng)
κ 450 (50ng)
κ 450 (100ng)
κ 450 (200ng)
1 2 3 4 5 6 7 8 9 10 11

FIG.9B

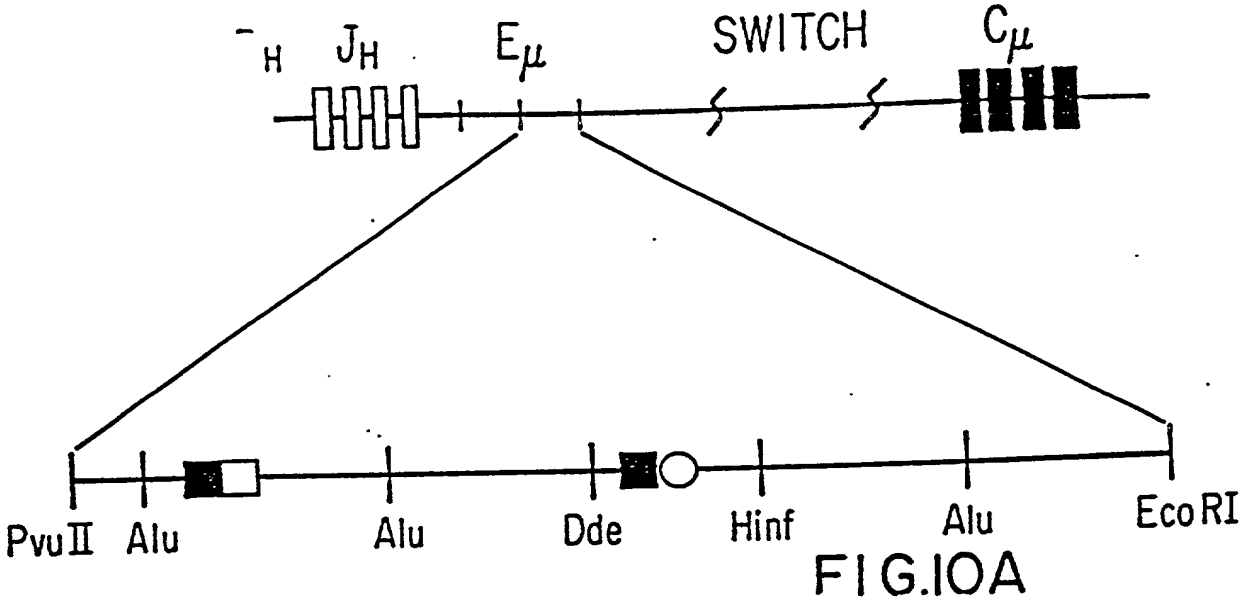


FIG.10A

■ : E

□ : ?

○ : Octamer (ATTTGCAT)

FIG.10B

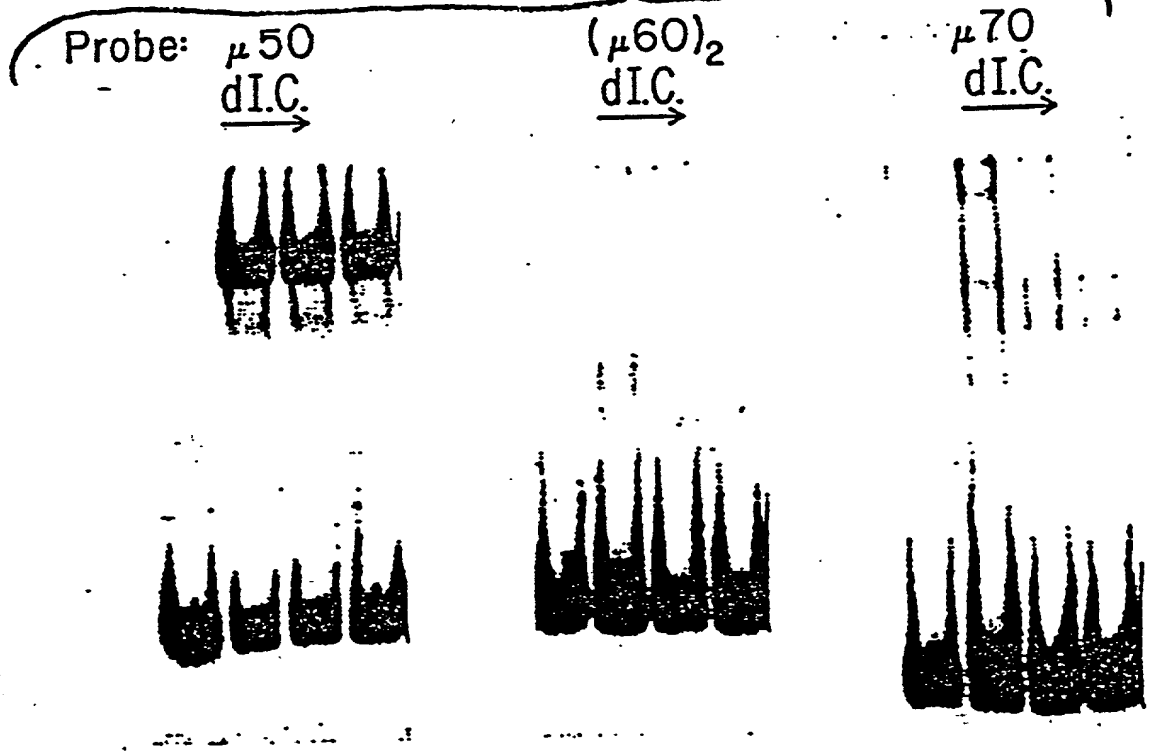
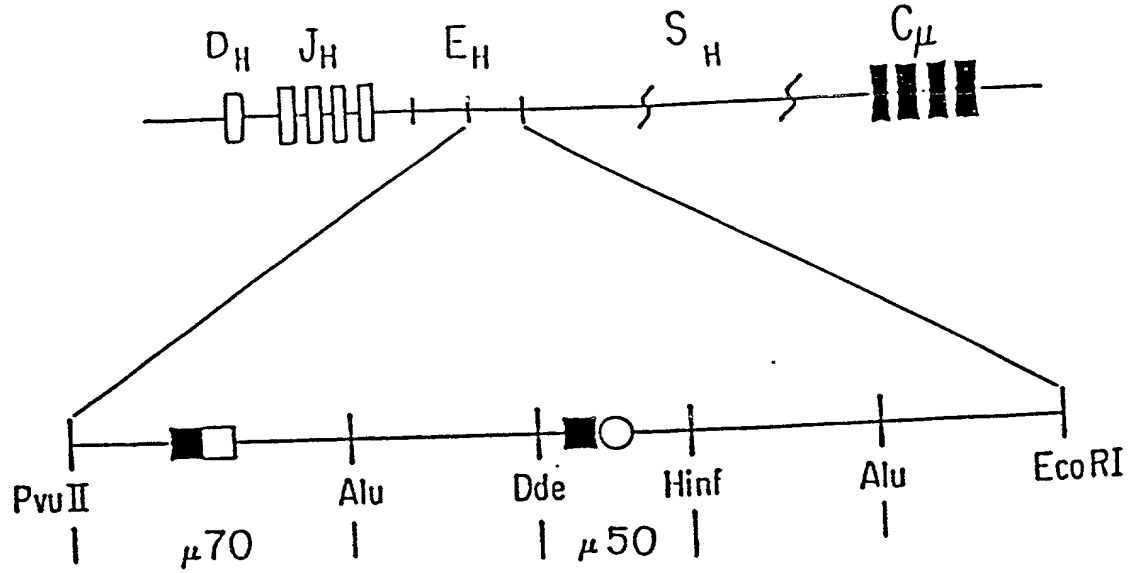


FIG.10C



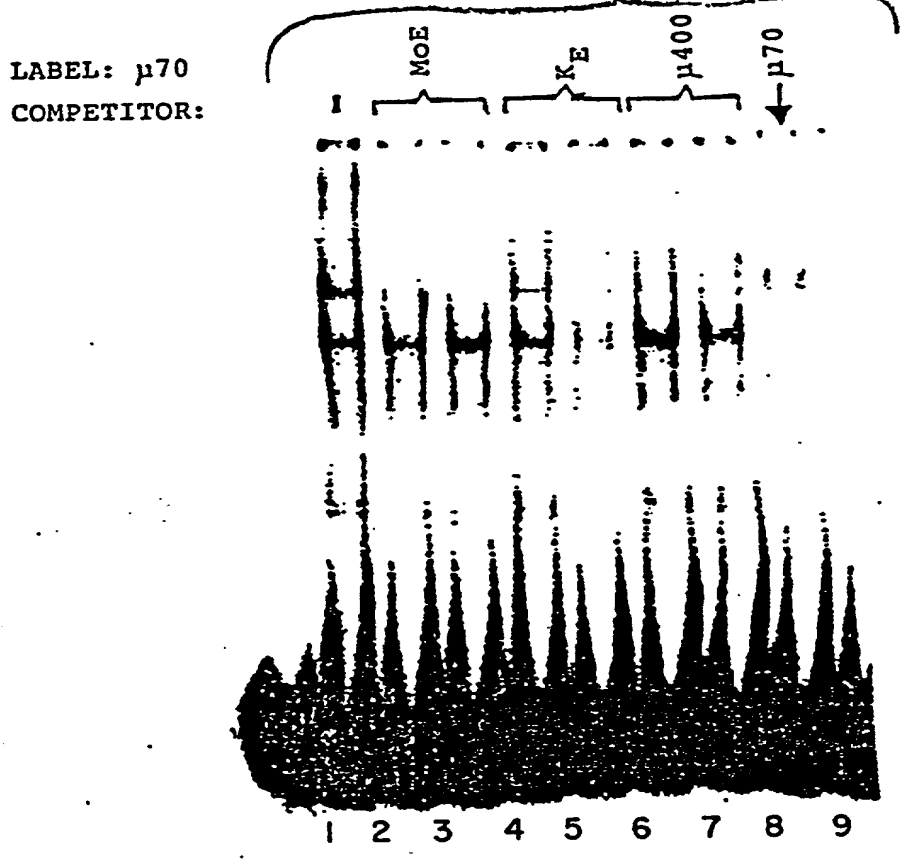
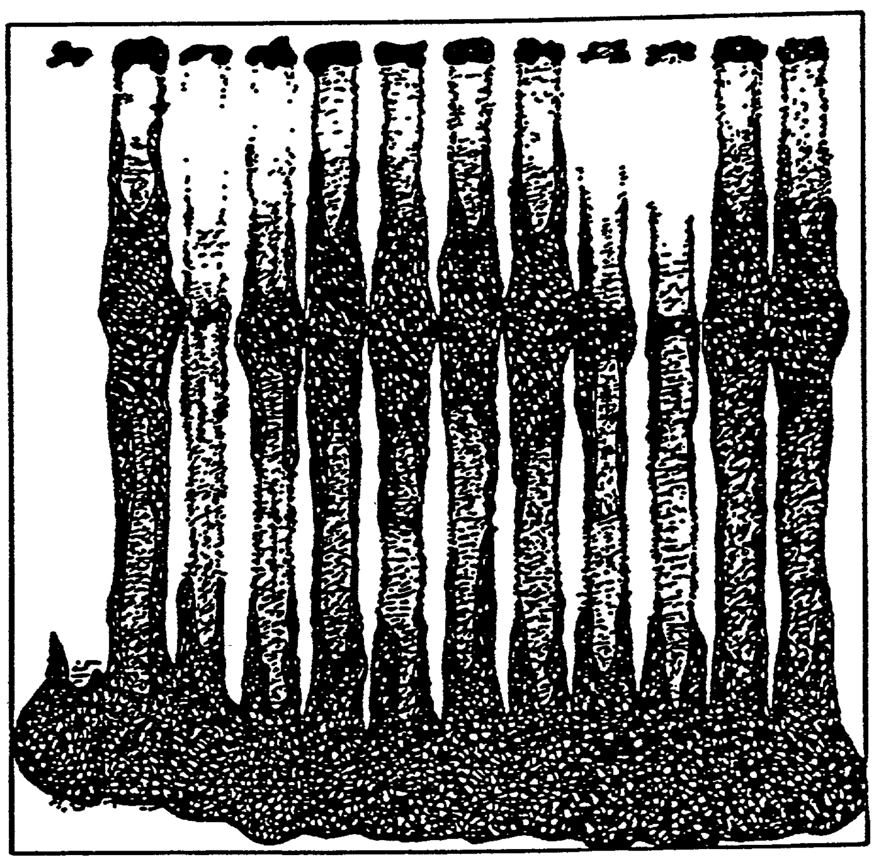


FIG.10D

FIG.10E



Probe: μ70
Extract : EW(C)
Competitor
-
-
μ300 (50 ng)
μ400 (50 ng)
μ50 (10 ng)
μ50 (30 ng)
μ60 (10 ng)
μ60 (30 ng)
μ70 (10 ng)
μ70 (30 ng)
μ170 (20 ng)
μ170 (60 ng)
1 2 3 4 5 6 7 8 9 10 11 12

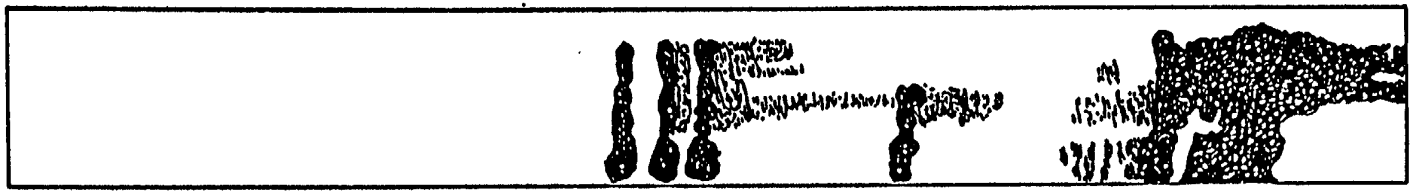


FIG.11A

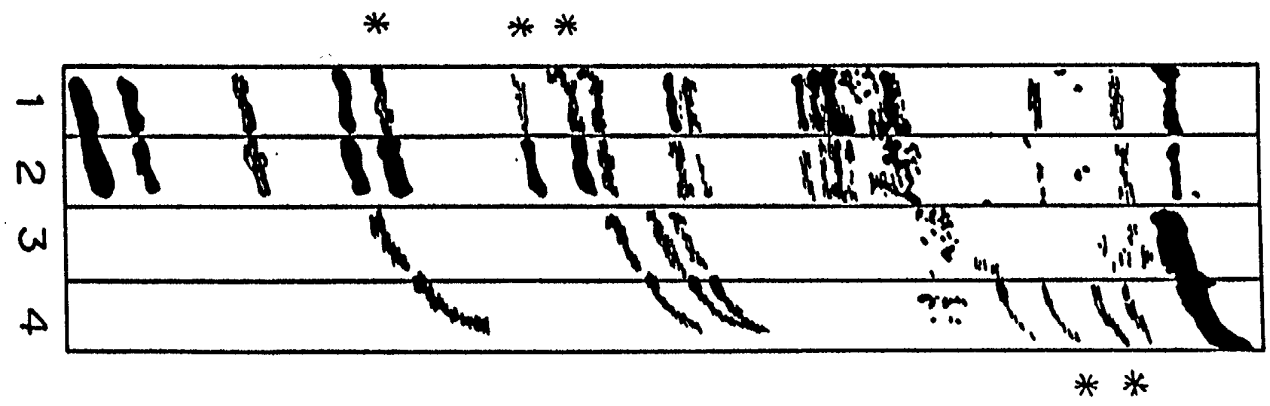


FIG.11B

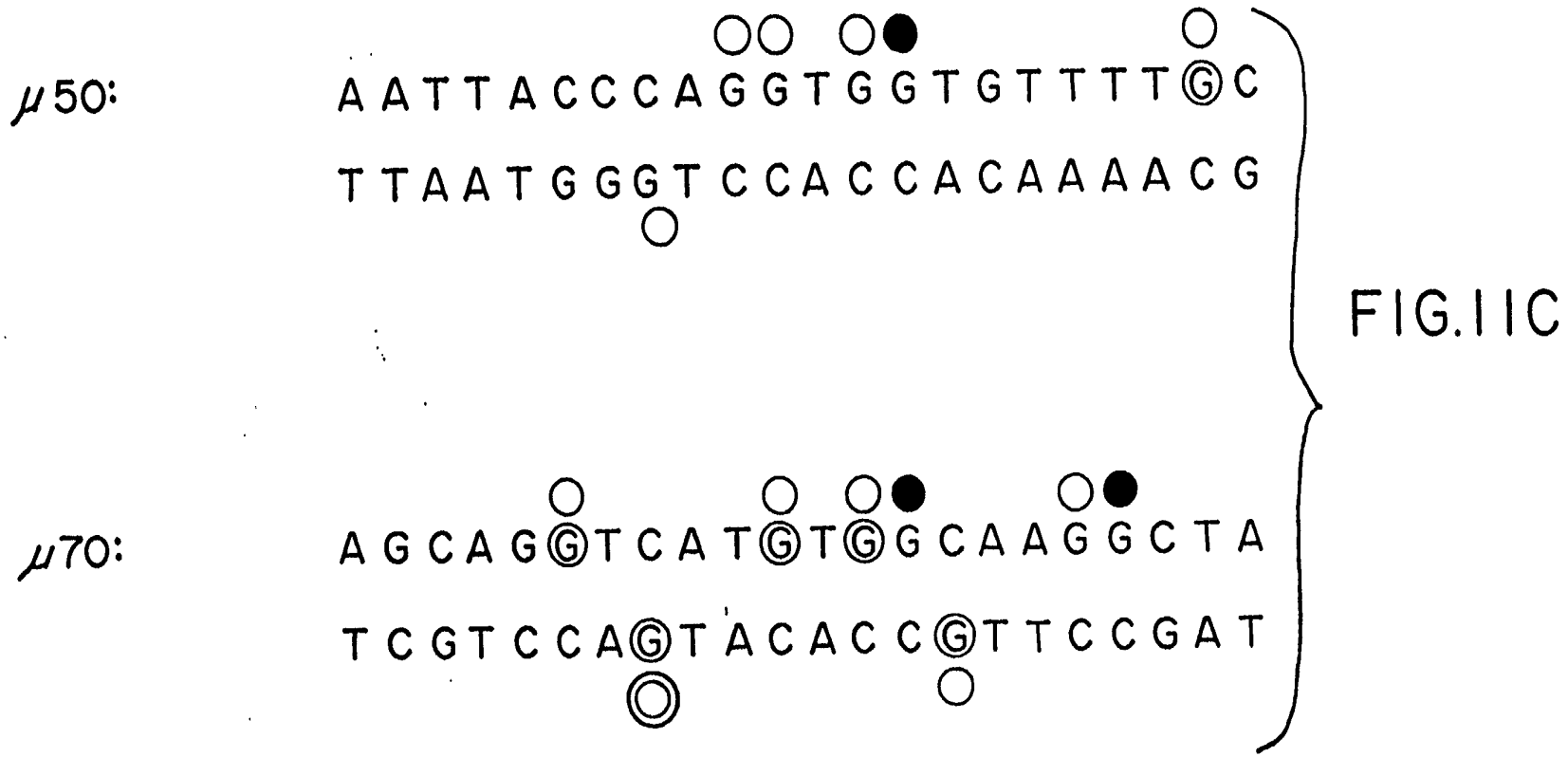
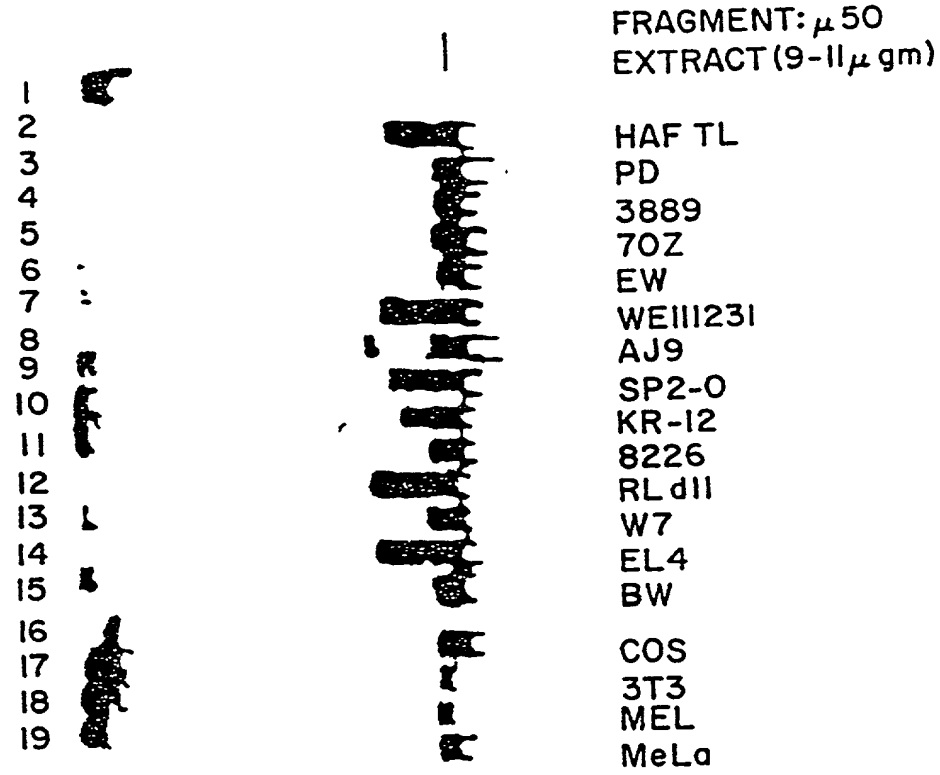


FIG.11C

FIG.12A



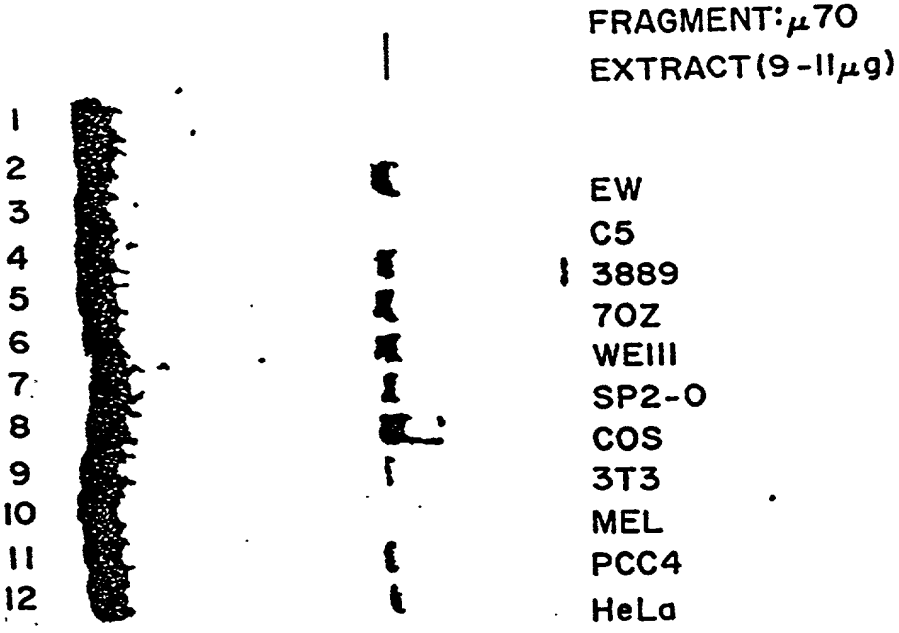


FIG.12B

FIG.13A

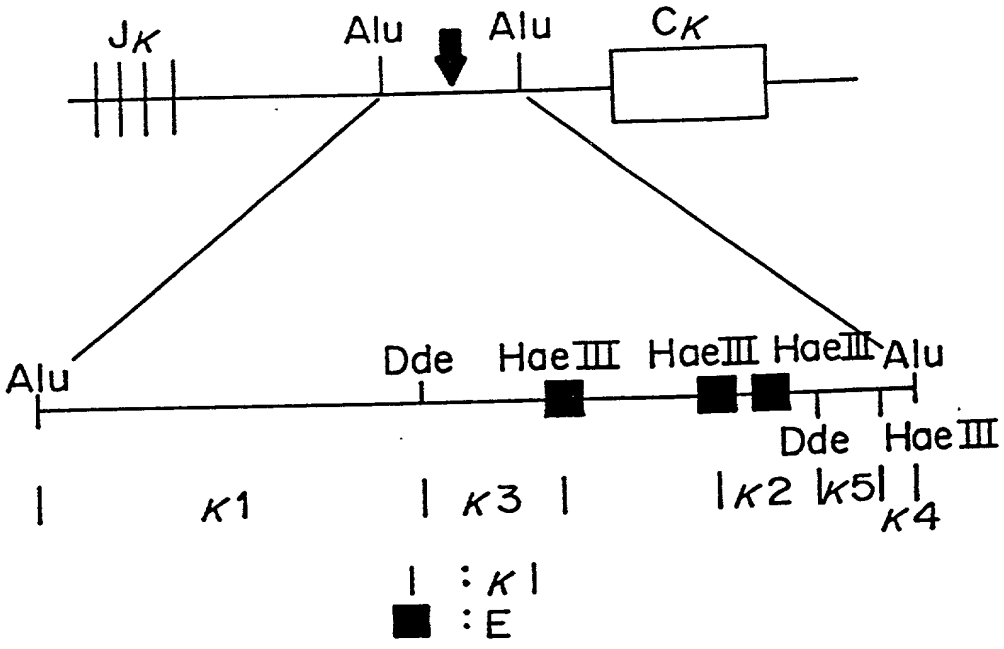
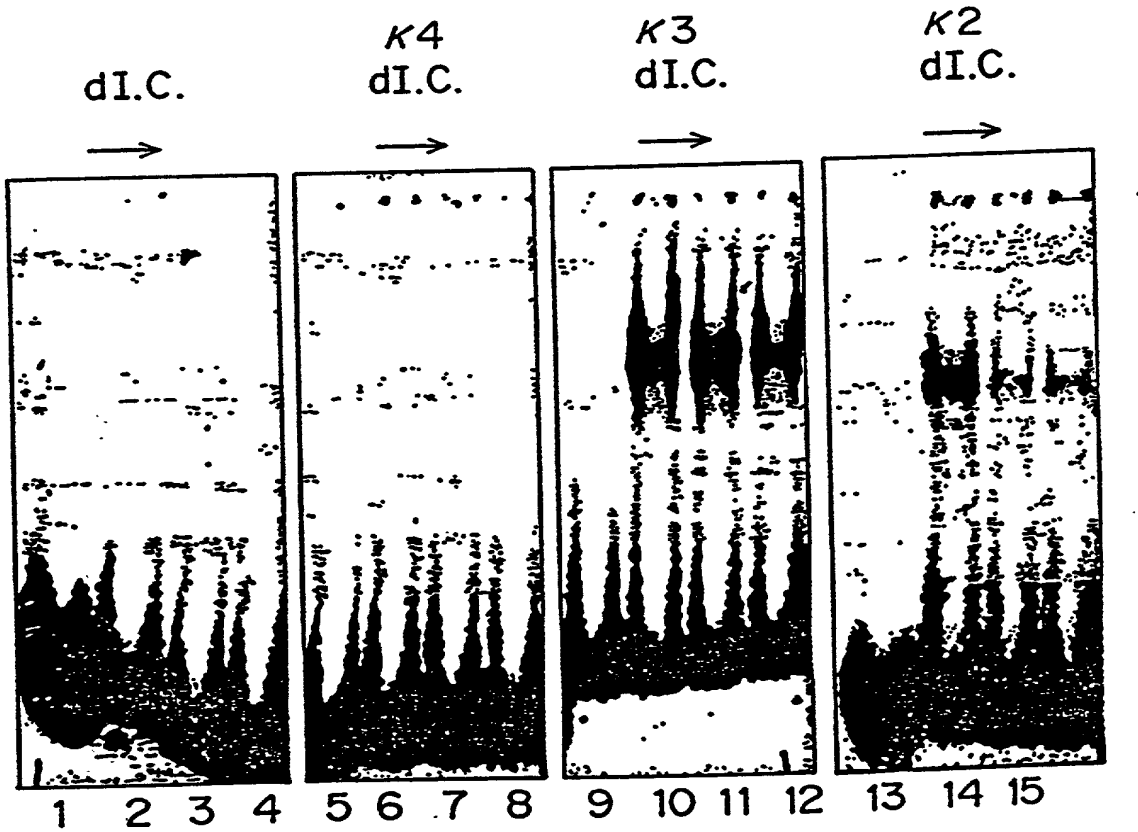
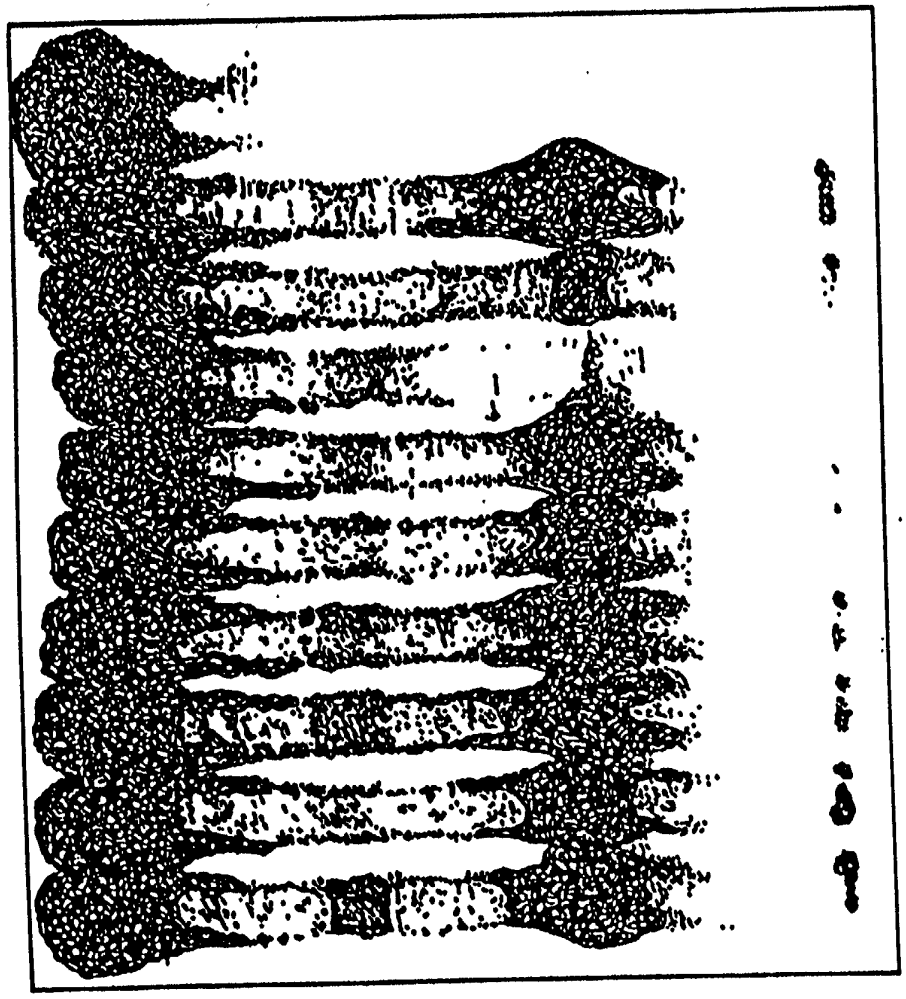


FIG.13B

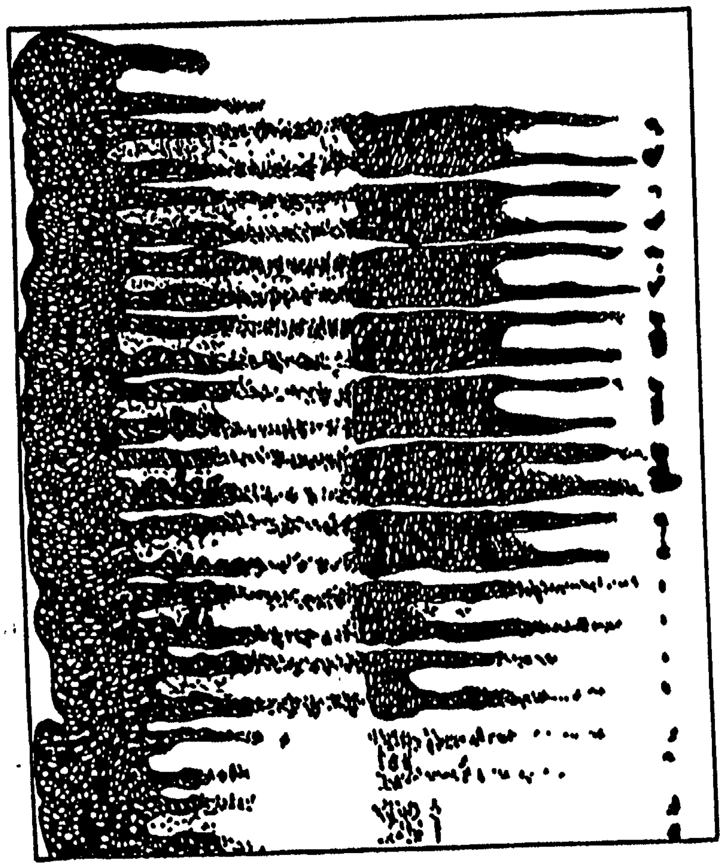




1 2 3 4 5 6 7 8 9 10

Extract fragment	EW/c 1 µl Comp
K2	–
K2	–
K2	M70 10ng
K2	M70 30ng
K2	$(M60)_2$ 10
K2	$(M60)_2$ 30
K2	$(M170)_2$ 20
K2	M170 60
K2	SV40E 50
K2	SV40E 150

FIG.13C



Probe: κ3

Extract : EW/N

Competitor

-

-

μ300 (50ng)

μ300 (150ng)

μ400 (50ng)

μ400 (150 ng)

κpr (50 ng)

κpr (150ng)

κ450 (50ng)

κ450 (150ng)

SV40E (50ng)

SV40E (150ng)

FIG.13D

FIG.14

FIG.15A

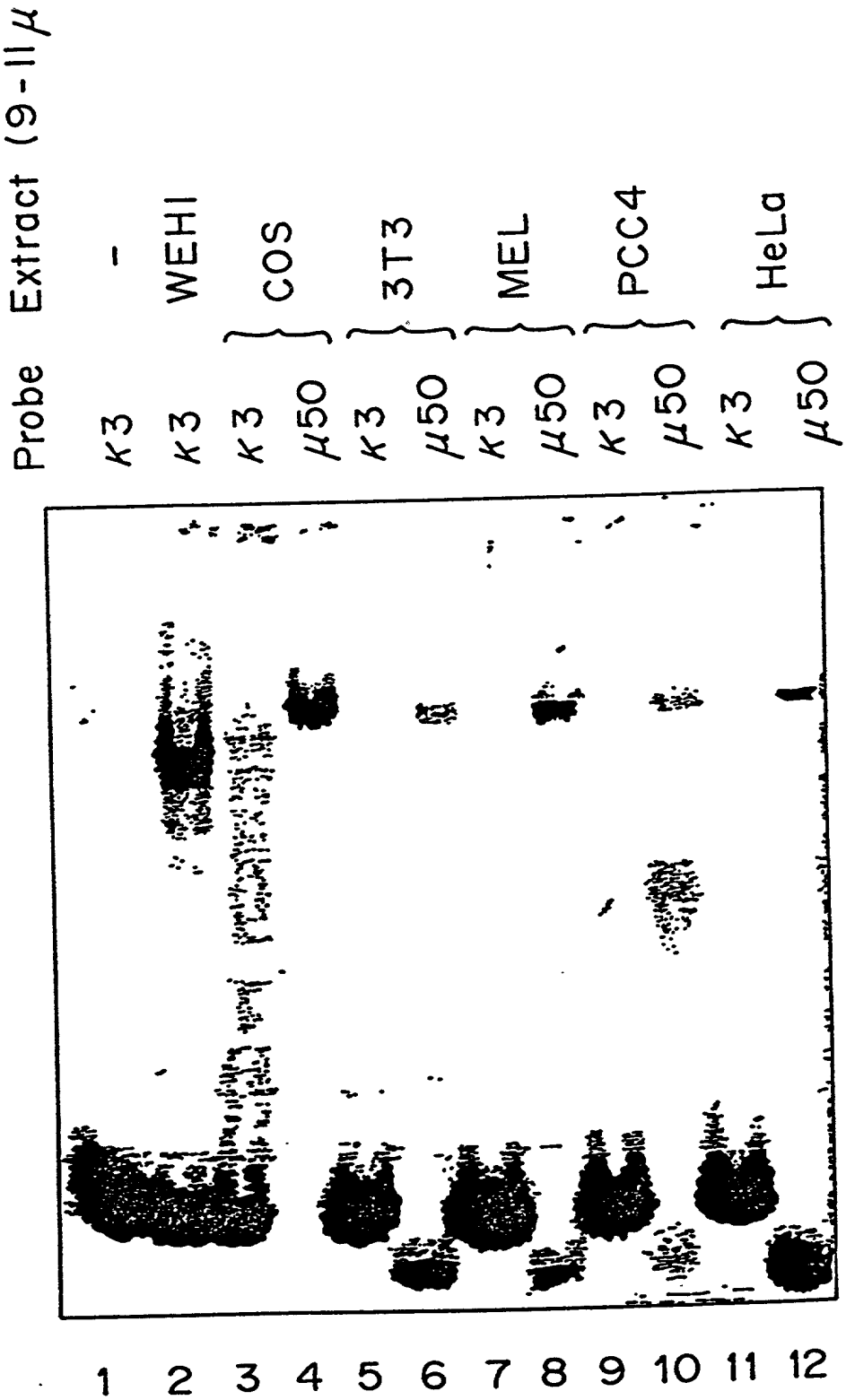

Probe
Extract (9-11μ
κ3
-
κ3
WEHI
κ3
COS
μ50
κ3
3T3
μ50
κ3
MEL
μ50
κ3
PCC4
μ50
κ3
HeLa
μ50
1 2 3 4 5 6 7 8 9 10 11 12

FIG.15B

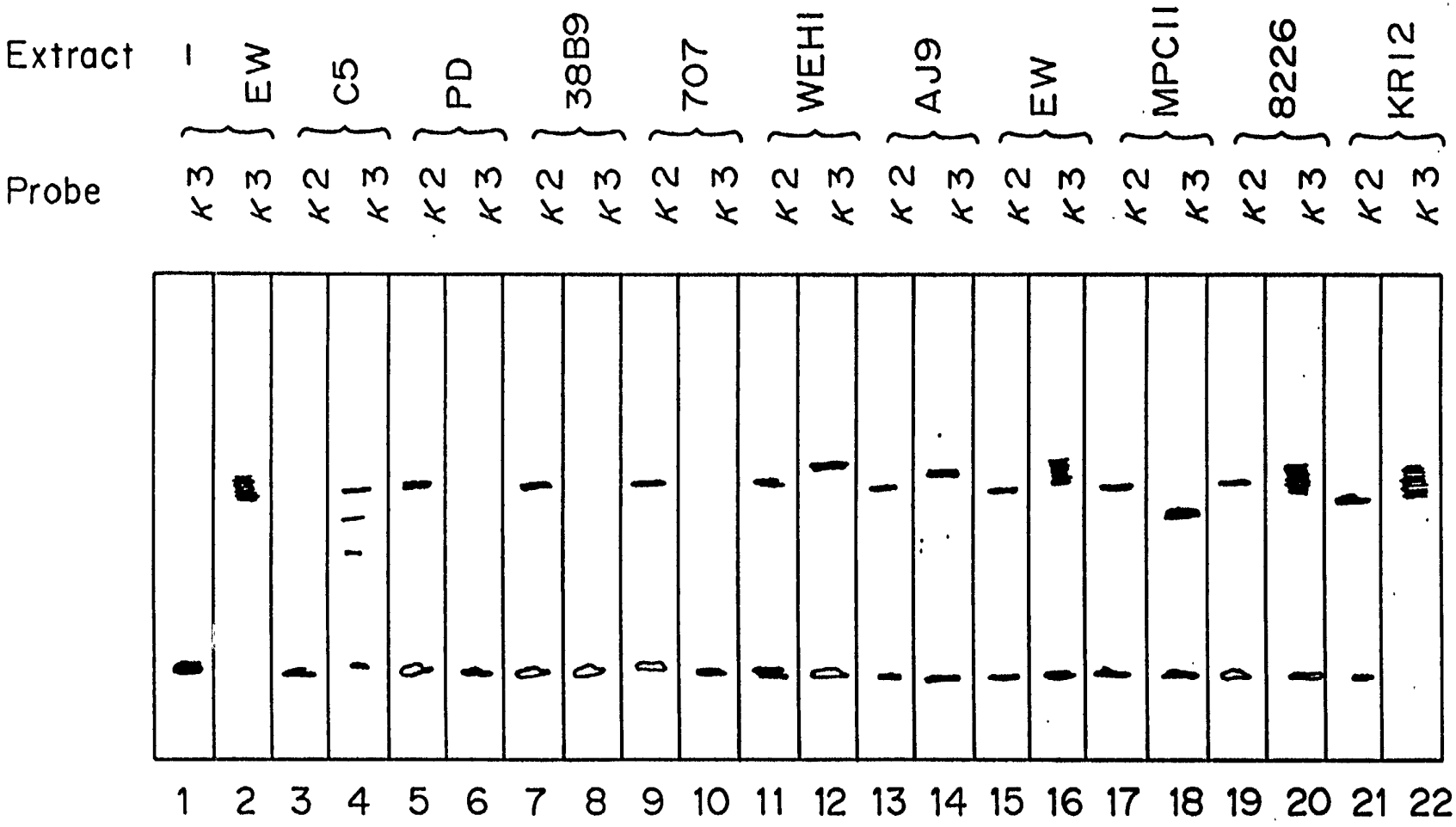


FIG.16

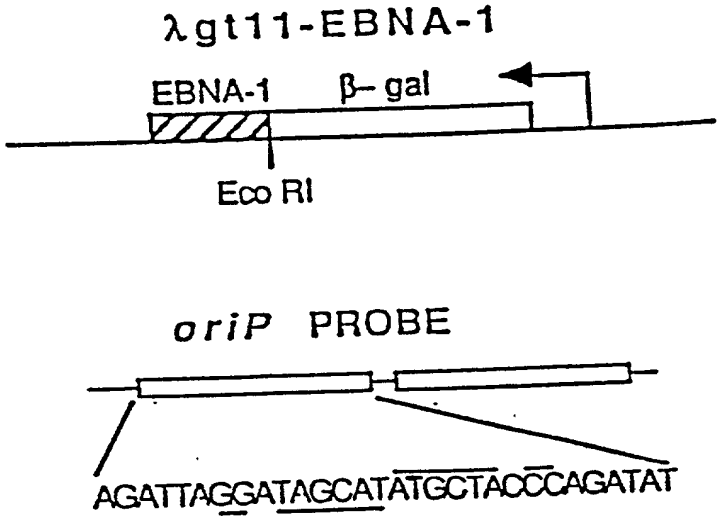

λgt11-EBNA-1
EBNA-1
β- gal
Eco RI
oriP PROBE
AGATTAGGATAGCATATGCTACCCAGATAT
EBNA-1 CONSENSUS BINDING SITE

FIG.17

A.

MHC	TGGGGATTCCCCA
mhc1	TGcGGATTCCCaA
κEN	aGGGGAcTttCCg
κen	aaattaAcTttCCg
SVEN	TGGGGAcTttCCA
HIV	TGGGGAcTttCCA
	aaGGGAcTttCCg

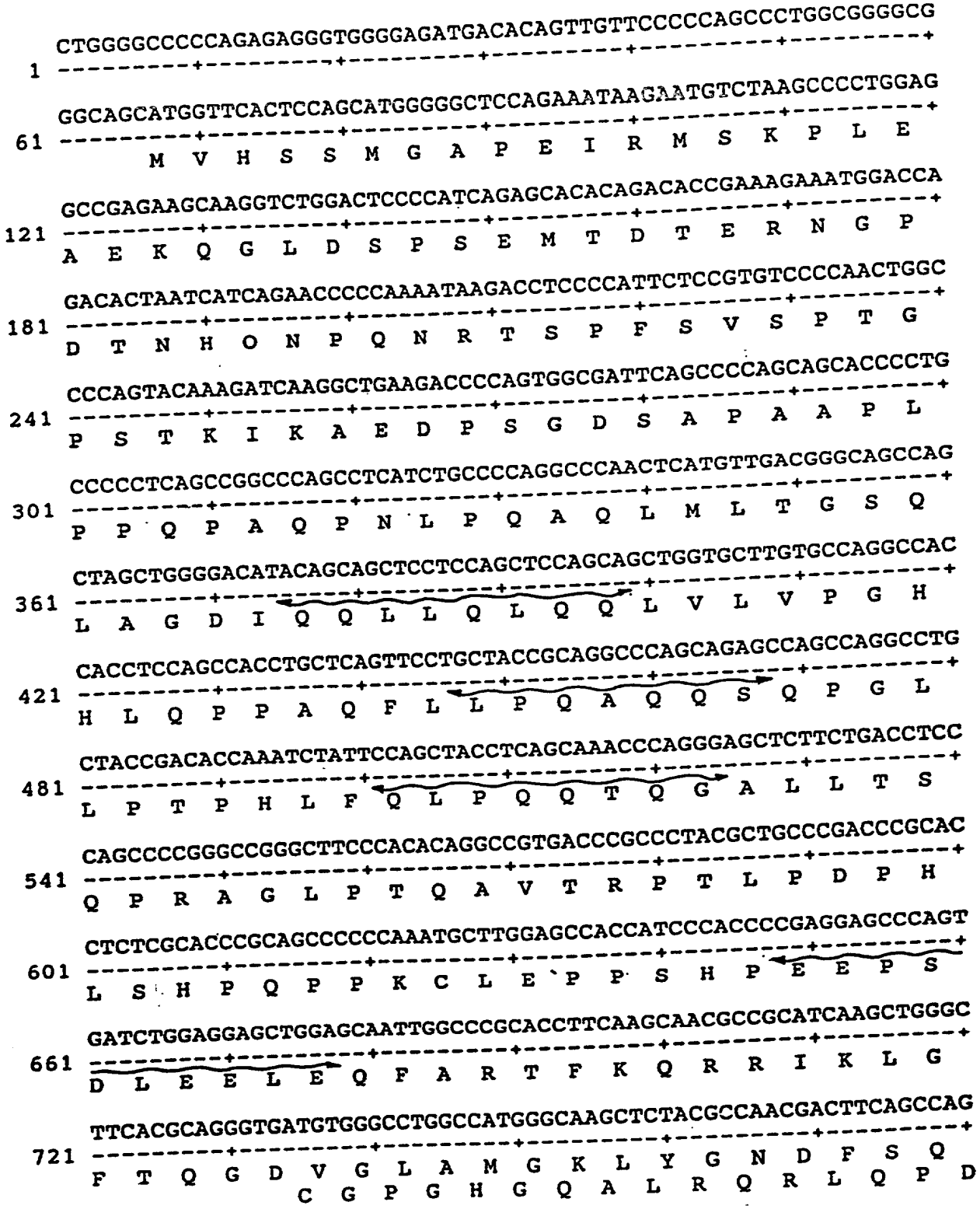

CTGGGGCCCCCAGAGAGGGTGGGGAGATGACACAGTTGTTCCCCCAGCCCTGGCGGGGCG
1
GGCAGCATGGTTCACTCCAGCATGGGGGCTCCAGAAATAAGAATGTCTAAGCCCCTGGAG
61
M V H S S M G A P E I R M S K P L E
GCCGAGAAGCAAGGTCTGGACTCCCCATCAGAGCACACAGACACCGAAAGAAATGGACCA
121
A E K Q G L D S P S E M T D T E R N G P
GACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTCTCCGTGTCCCCAACTGGC
181
D T N H O N P Q N R T S P F S V S P T G
CCCAGTACAAAGATCAAGGCTGAAGACCCCAGTGGCGATTCAGCCCCAGCAGCACCCCTG
241
P S T K I K A E D P S G D S A P A A P L
CCCCCTCAGCCGGCCCAGCCTCATCTGCCCCAGGCCCAACTCATGTTGACGGGCAGCCAG
301
P P Q P A Q P N L P Q A Q L M L T G S Q
CTAGCTGGGGACATACAGCAGCTCCTCCAGCTCCAGCAGCTGGTGCTTGTGCCAGGCCAC
361
L A G D I Q Q L L Q L Q Q L V L V P G H
CACCTCCAGCCACCTGCTCAGTTCCTGCTACCGCAGGCCCAGCAGAGCCAGCCAGGCCTG
421
H L Q P P A Q F L L P Q A Q Q S Q P G L
CTACCGACACCAAATCTATTCCAGCTACCTCAGCAAACCCAGGGAGCTCTTCTGACCTCC
481
L P T P H L F Q L P Q Q T Q G A L L T S
CAGCCCCGGGCCGGGCTTCCCACACAGGCCGTGACCCGCCCTACGCTGCCCGACCCGCAC
541
Q P R A G L P T Q A V T R P T L P D P H
CTCTCGCACCCGCAGCCCCCCAAATGCTTGGAGCCACCATCCCACCCCGAGGAGCCCAGT
601
L S H P Q P P K C L E P P S H P E E P S
GATCTGGAGGAGCTGGAGCAATTGGCCCGCACCTTCAAGCAACGCCGCATCAAGCTGGGC
661
D L E E L E Q F A R T F K Q R R I K L G
TTCACGCAGGGTGATGTGGGCCTGGCCATGGGCAAGCTCTACGCCAACGACTTCAGCCAG
721
F T Q G D V G L A M G K L Y G N D F S Q
C G P G H G Q A L R Q R L Q P D

FIG. 18A

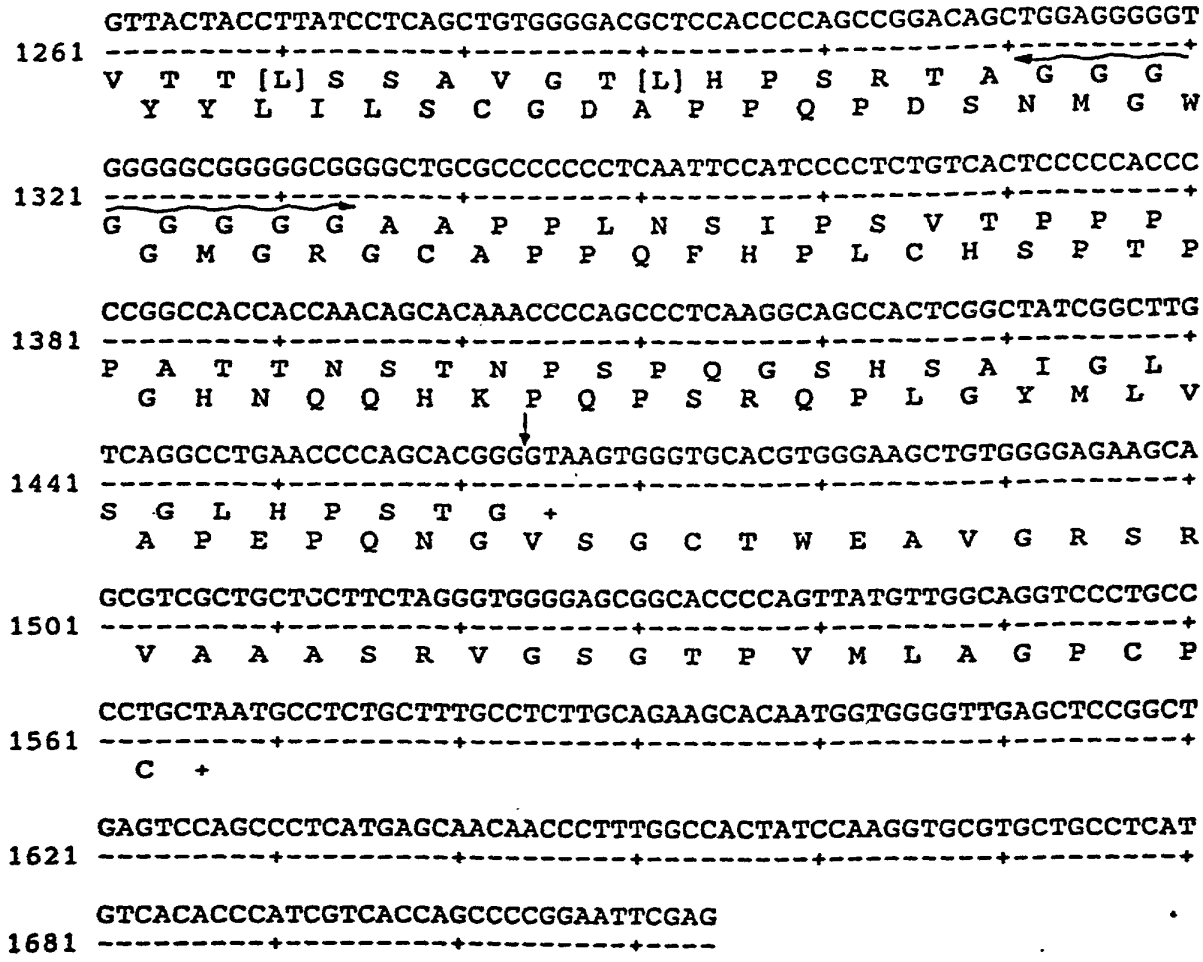

GTTACTACCTTATCCTCAGCTGTGGGGACGCTCCACCCCAGCCGGACAGCTGGAGGGGGT
1261
V T T [L] S S A V G T [L] H P S R T A G G G
Y Y L I L S C G D A P P Q P D S N M G W
GGGGGCGGGGGCGGGGCTGCGCCCCCCCTCAATTCCATCCCCTCTGTCACTCCCCCACCC
1321
G G G G G A A P P L N S I P S V T P P P
G M G R G C A P P Q F H P L C H S P T P
CCGGCCACCACCAACAGCACAAACCCCAGCCCTCAAGGCAGCCACTCGGCTATCGGCTTG
1381
P A T T N S T N P S P Q G S H S A I G L
G H N Q Q H K P Q P S R Q P L G Y M L V
TCAGGCCTGAACCCCAGCACGGGGTAAGTGGGTGCACGTGGGAAGCTGTGGGGAGAAGCA
1441
S G L H P S T G +
A P E P Q N G V S G C T W E A V G R S R
GCGTCGCTGCTCCTTCTAGGGTGGGGAGCGGCACCCCAGTTATGTTGGCAGGTCCCTGCC
1501
V A A A S R V G S G T P V M L A G P C P
CCTGCTAATGCCTCTGCTTTGCCTCTTGCAGAAGCACAATGGTGGGGTTGAGCTCCGGCT
1561
C +
GAGTCCAGCCCTCATGAGCAACAACCCTTTGGCCACTATCCAAGGTGCGTGCTGCCTCAT
1621
GTCACACCCATCGTCACCAGCCCCGGAATTCGAG
1681

FIG.18A (CONT.)

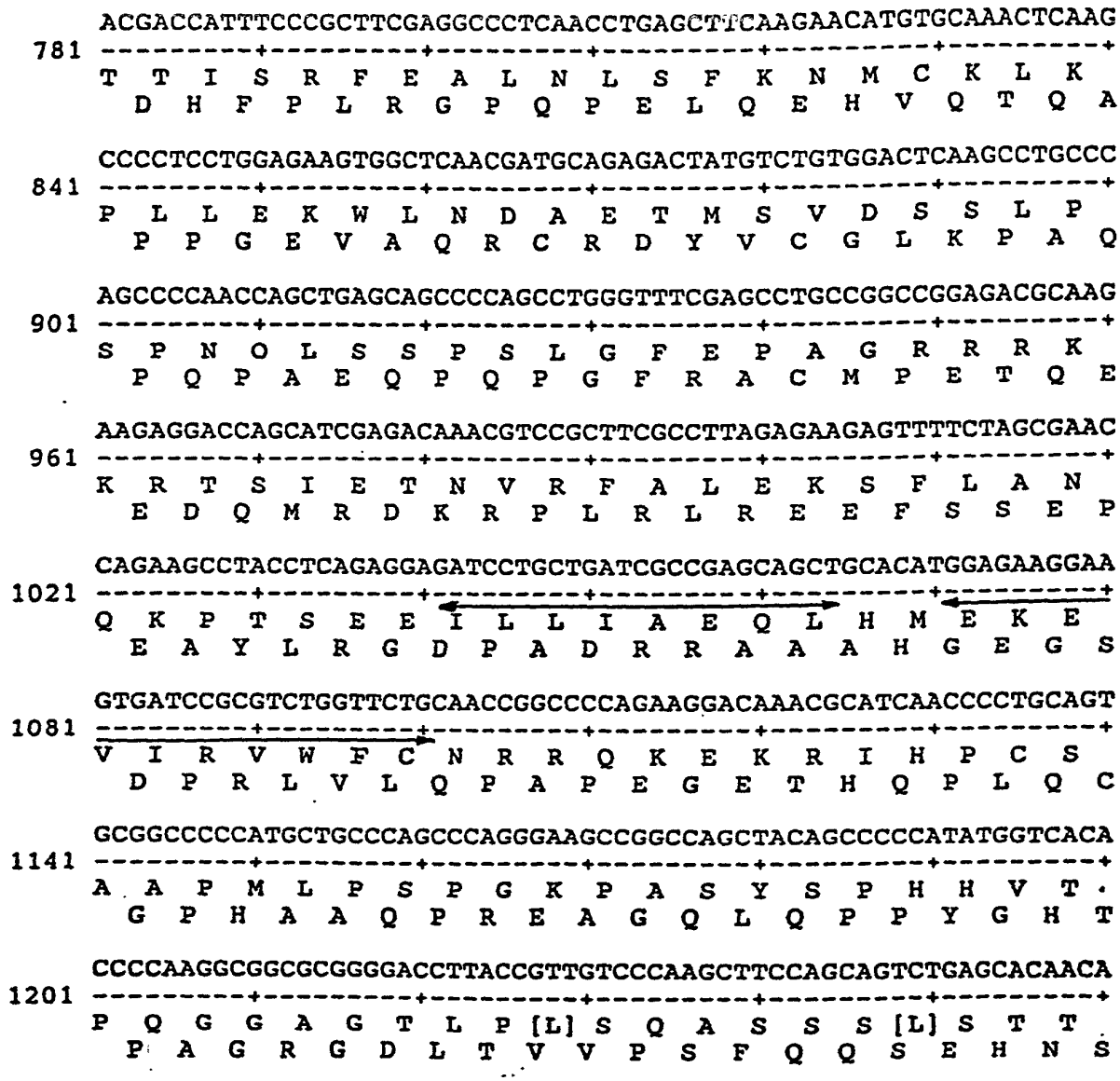


FIG.18A (CONT.)

```
     CCTCAAGGCAGCCACTCGGCTATCGGCTTGTCAGGCCTGAACCCCAGCACGGGCCCTGGC
1411 ---------+---------+---------+---------+---------+---------+
     P  Q  G  S  H  S  A  I  G  L  S  G  L  N  P  S  T  G  P  G
      S  A  Q  P  L  G  Y  R  L  V  M  P  E  P  Q  M  G  P  N  P

     CTCTGGTGGAACCCTGCCCCTTACCAGCCTTGATGGCAGCGGAATCTGGTGCTGGGGC
1471 ---------+---------+---------+---------+---------+---------+
     L  W  W  N  P  A  P  Y  Q  P  .
      L  V  E  P  C  P  L  P  A  L  M  A  A  G  I  W  C  W  G  Q

     AGCCGGTGCAGCCCCGGGGAGCCCTGGCCTGGTGACCTCGCCGCTCTTCTTGAATCATGC
1531 ---------+---------+---------+---------+---------+---------+
      P  V  Q  P  R  G  A  L  A  W  .

     TGGGCTGCCCCTGCTCAGCACCCCGCCTGGTGTGGGCCTGGTCTCAGCAGCGGCTGCGGG
1591 ---------+---------+---------+---------+---------+---------+

     TGTGGCAGCCTCCATCTCCAGCAAGTCTCCTGGCCTCTCCTCCTCATCCTCTTCATCCTC
1651 ---------+---------+---------+---------+---------+---------+

     ATCCTCCTCCTCCTCCACTTGCAGCGAGACGGCAGCACAGACCCTGGAGGTCCAGGGGGG
1711 ---------+---------+---------+---------+---------+---------+

     CCCGAGGCAGGGTCCAAACCTGAGTGAGGGCCAGCCATGCCTCCCCTCCCATTCCTCTGG
1771 ---------+---------+---------+---------+---------+---------+

     TCCCTGCCCCGGAATTC
1831 ---------+-------
```

FIG.18B

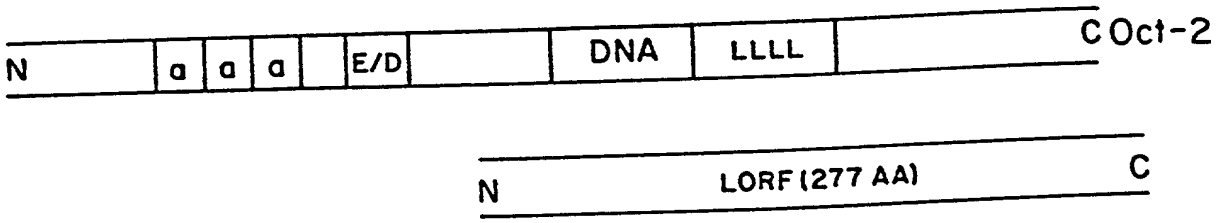


FIG.18C

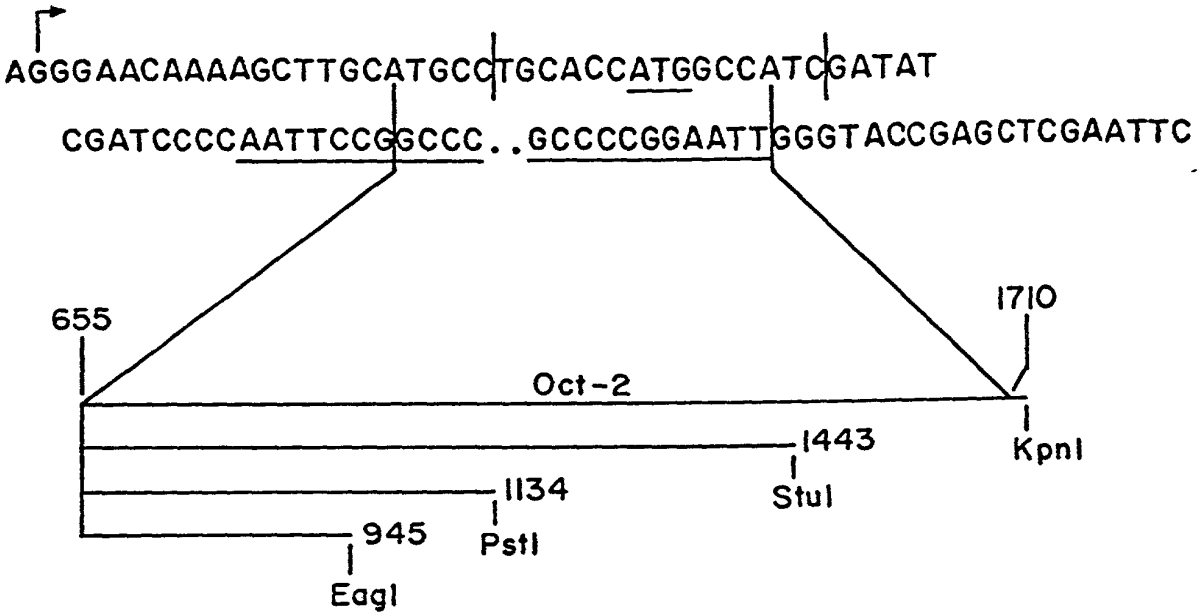

AGGGAACAAAAGCTTGCATGCCTGCACCATGGCCATCGATAT
CGATCCCCAATTCCGGCCC..GCCCCGGAATTGGGTACCGAGCTCGAATTC
655
1710
Oct-2
1443
KpnI
StuI
1134
PstI
945
EagI

FIG.19

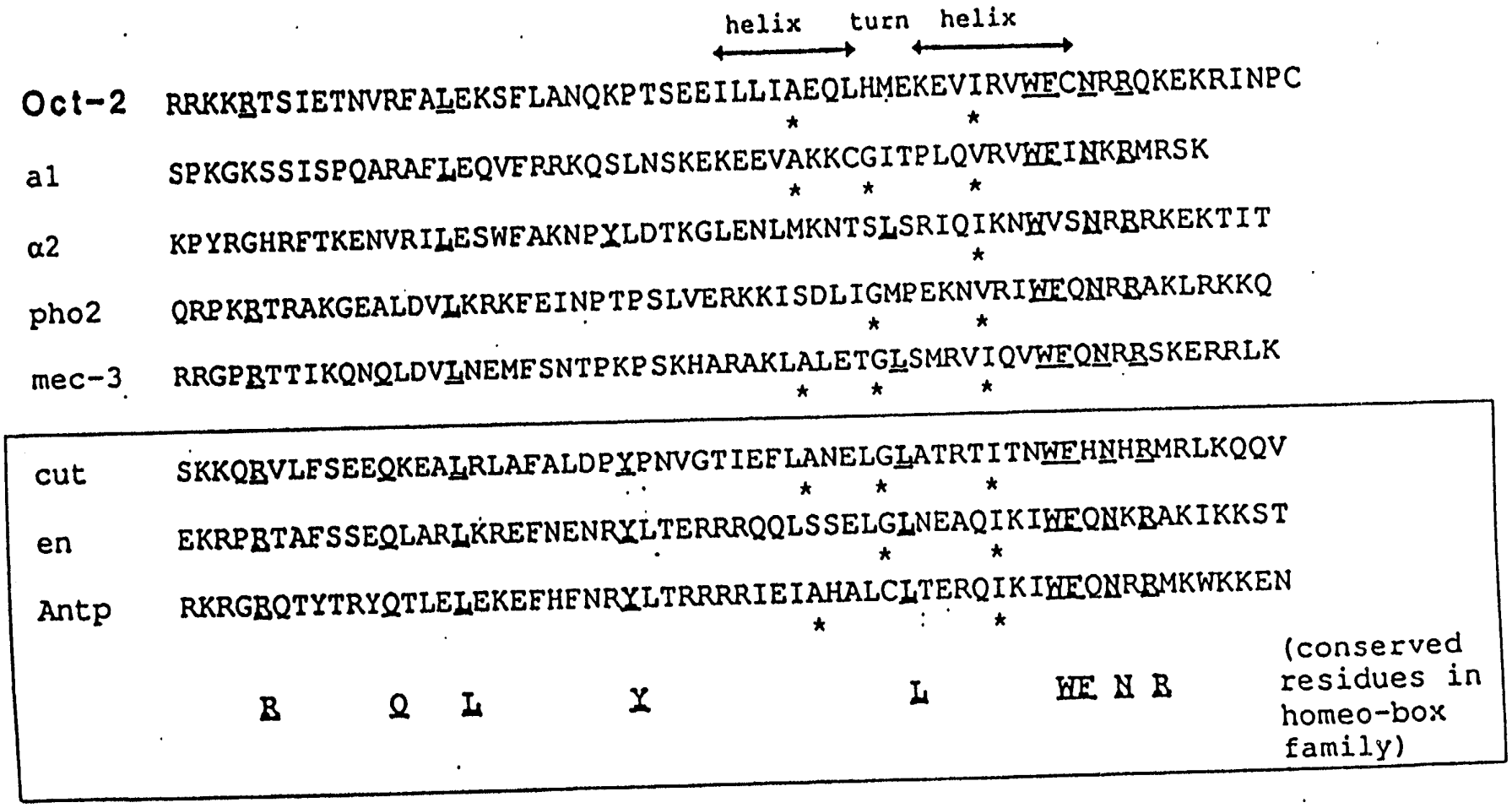
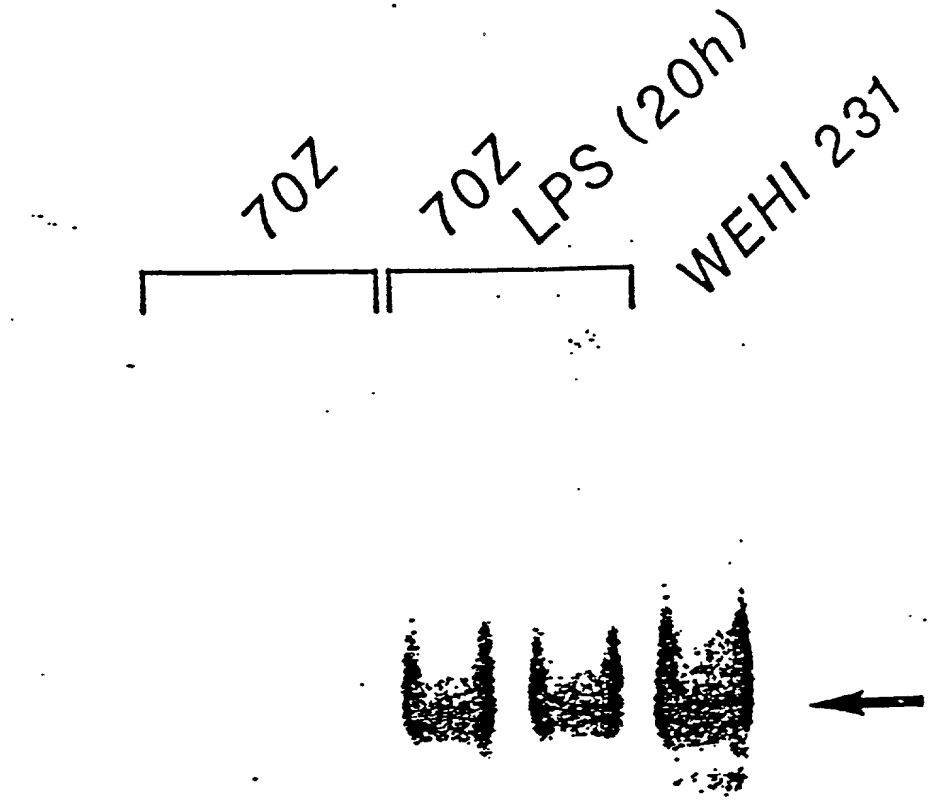


FIG.20

FIGURE 21A



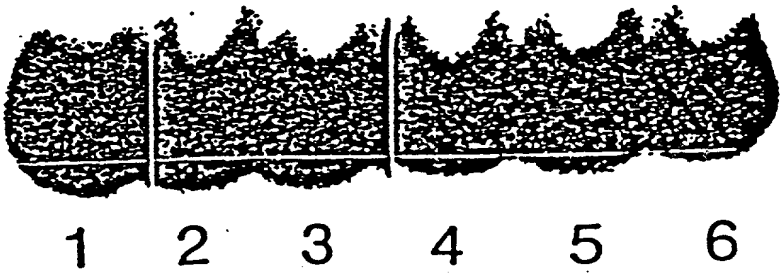


FIGURE 21B

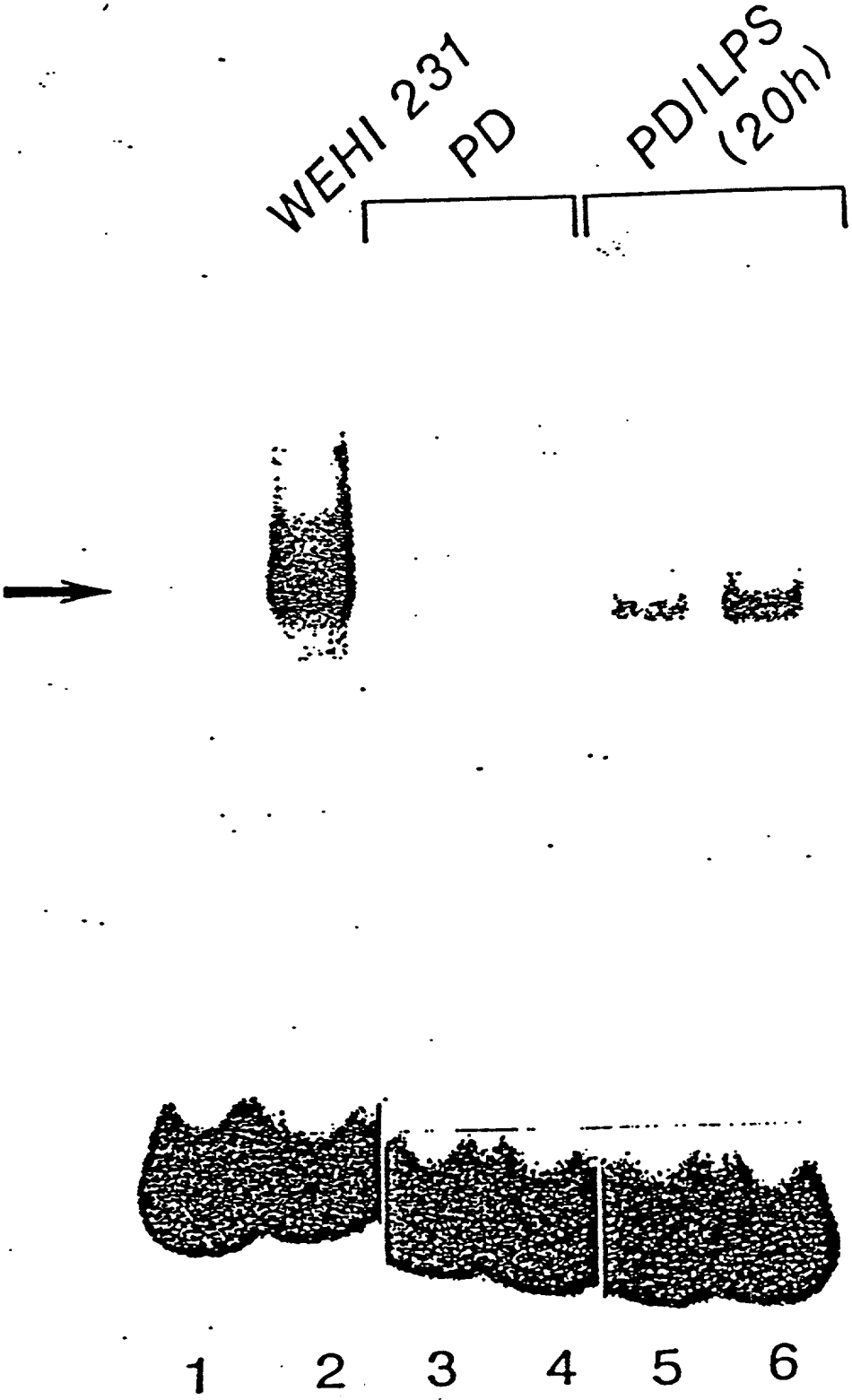


FIGURE 22A

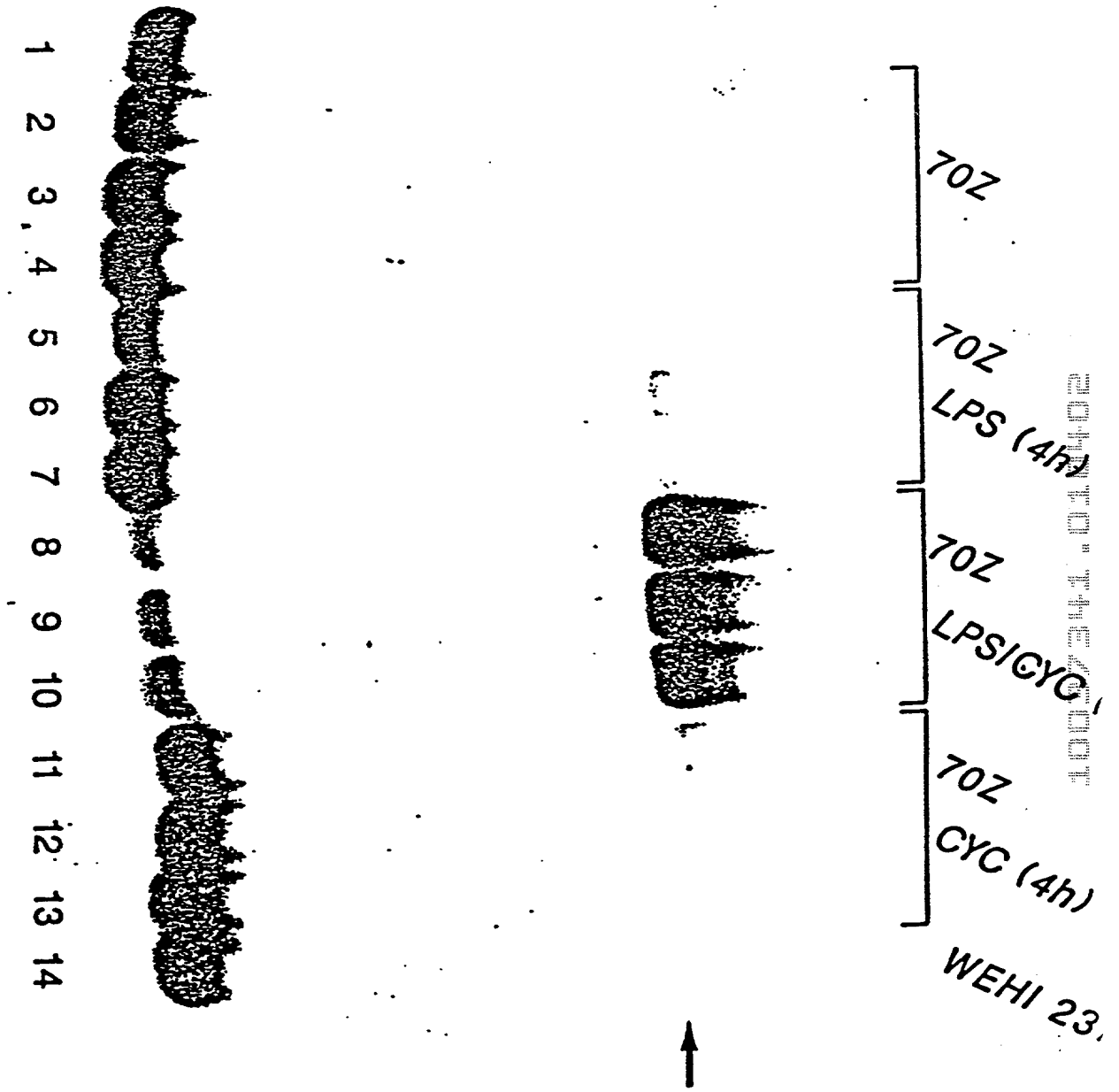

1 2 3 4 5 6 7 8 9 10 11 12 13 14
7OZ
7OZ LPS (4h)
7OZ LPS/CYC (4h)
7OZ CYC (4h)
WEHI 231

FIGURE 22B

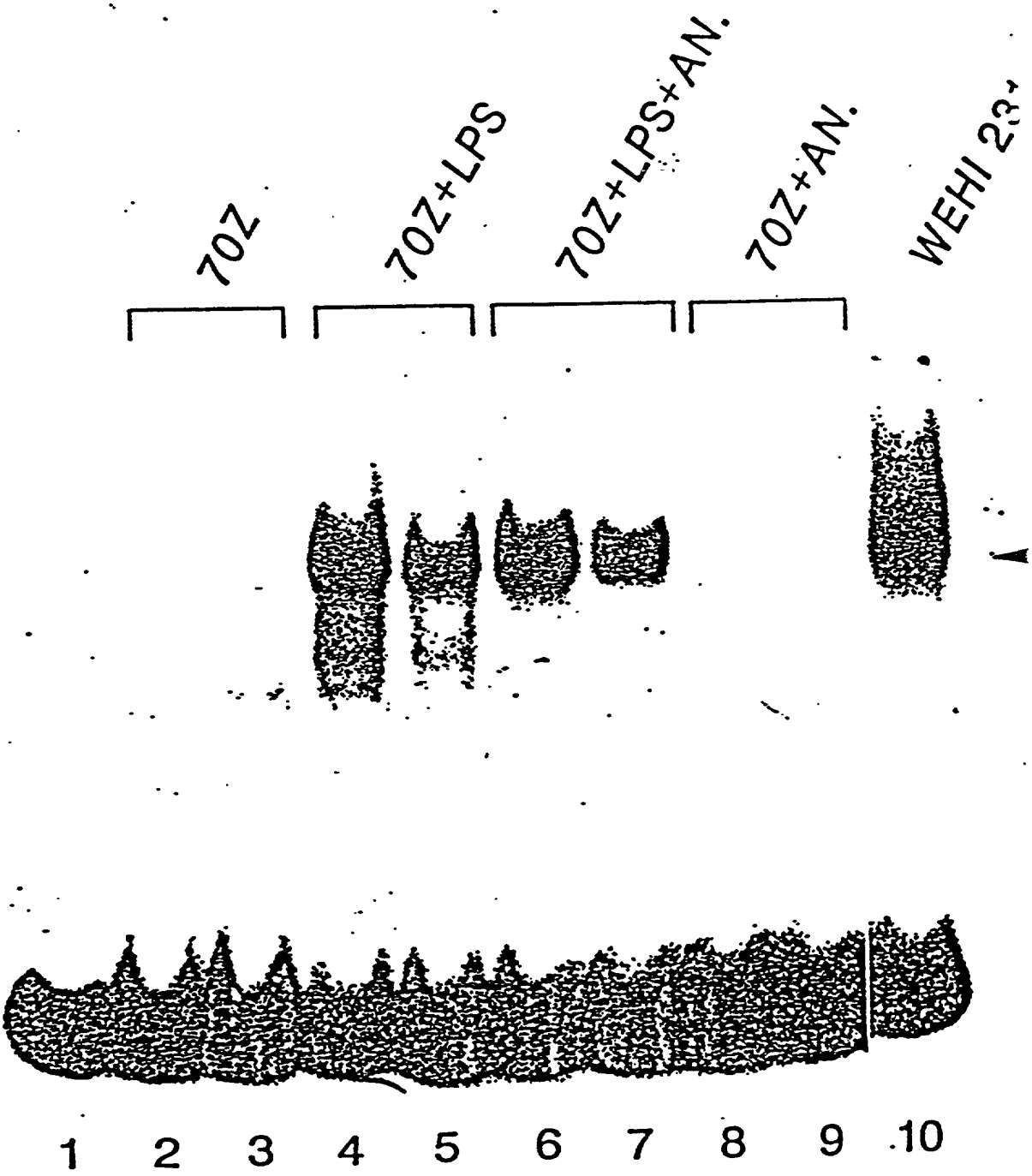


FIGURE 23A

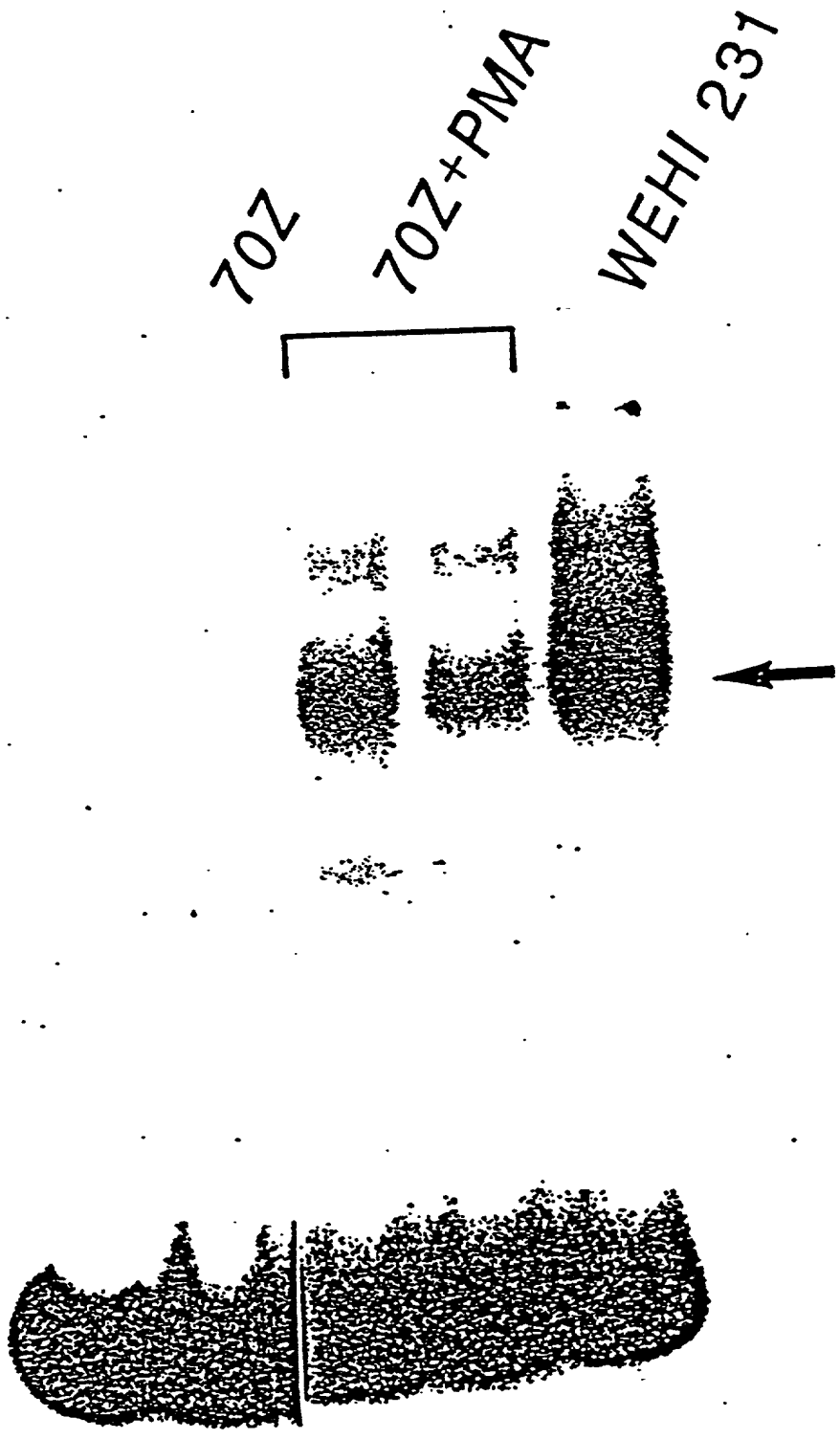


FIGURE 23B

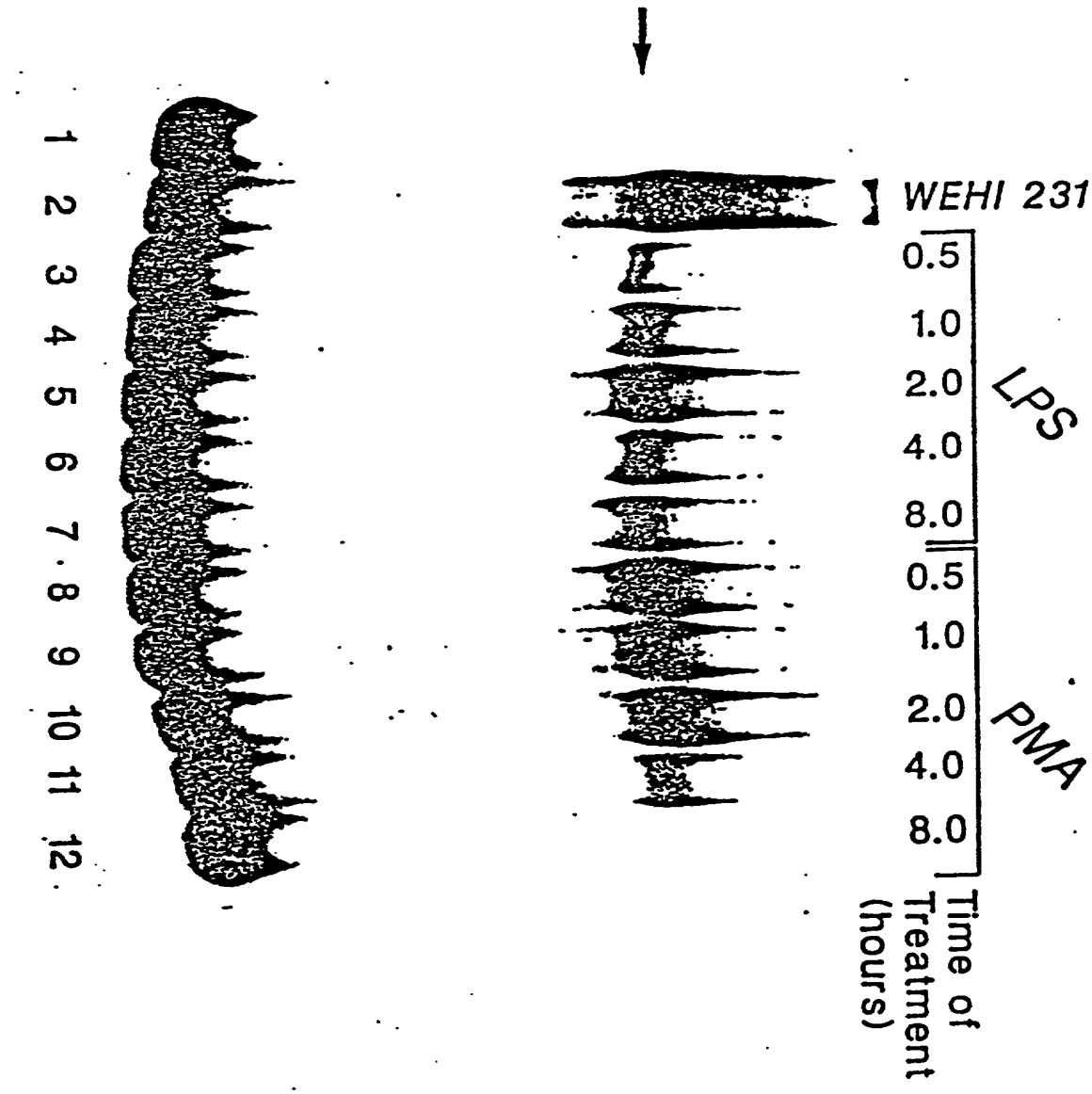

WEHI 231
0.5
1.0
2.0
4.0
8.0
LPS
0.5
1.0
2.0
4.0
8.0
PMA
Time of Treatment (hours)
1 2 3 4 5 6 7 8 9 10 11 12

FIGURE 24A

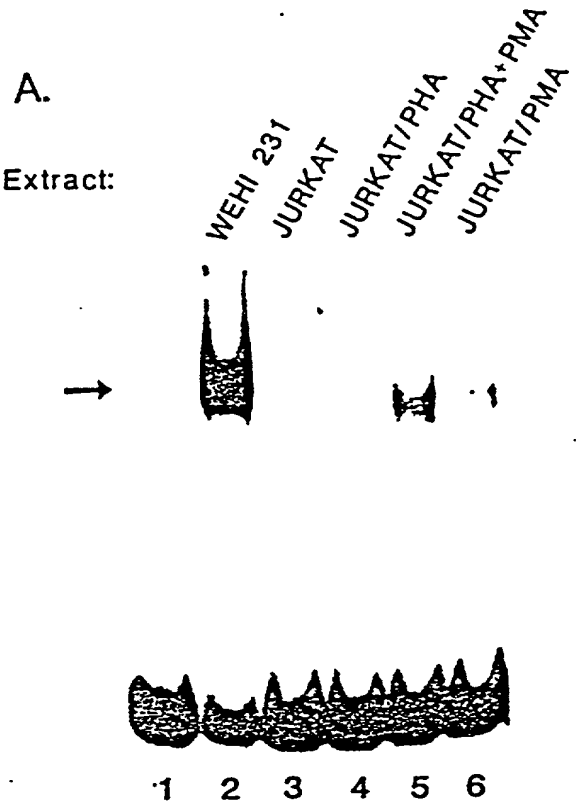


FIGURE 24B

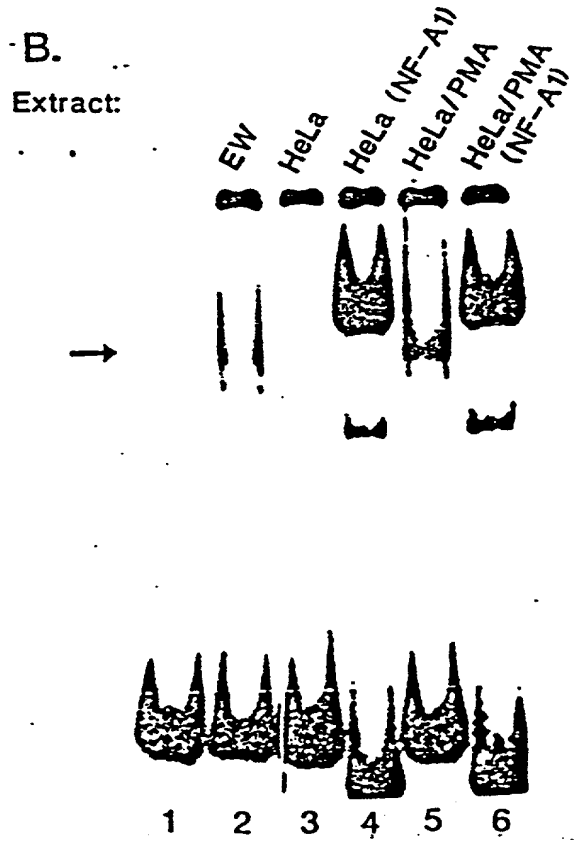


FIGURE 24C

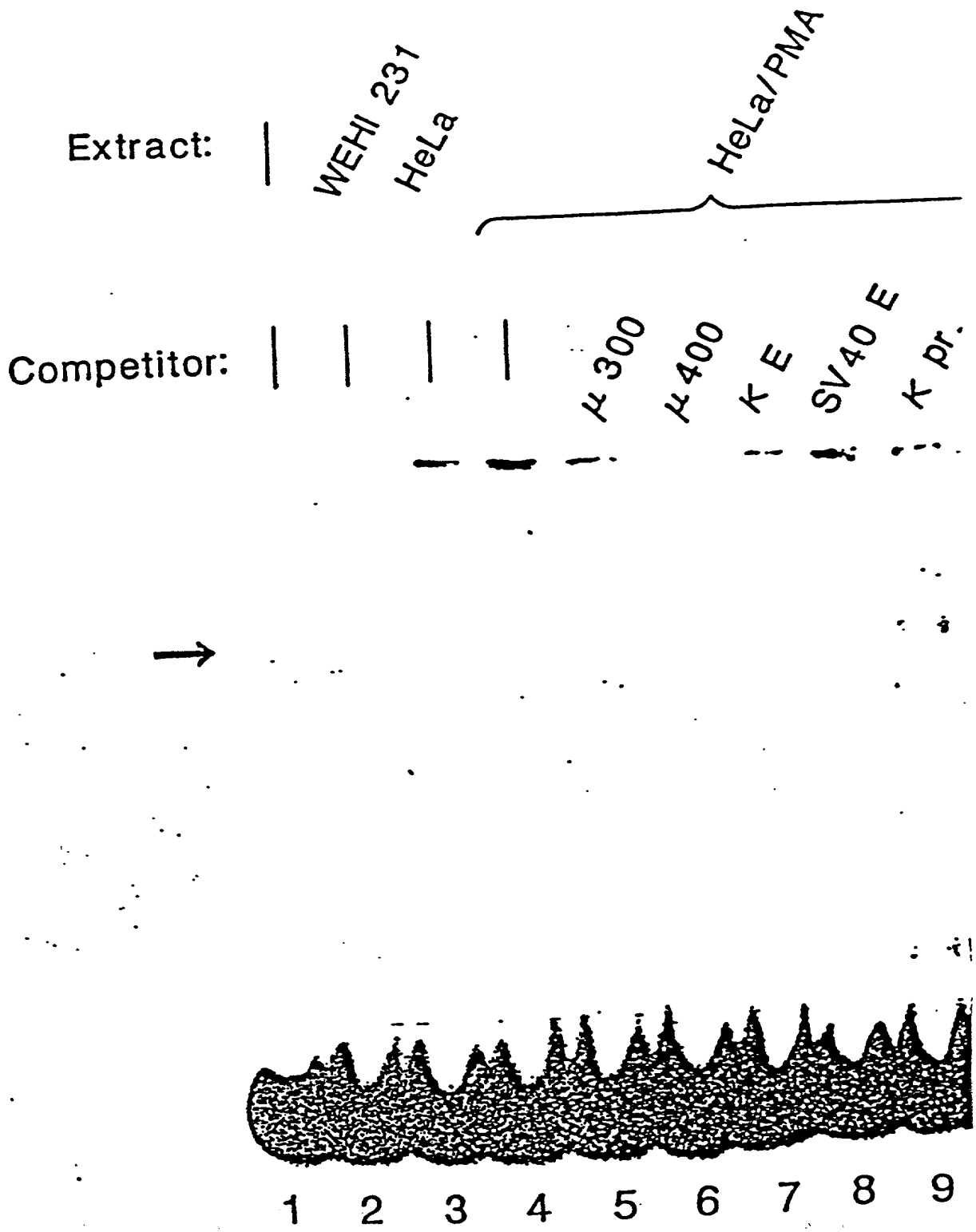

Extract:
WEHI 231
HeLa
HeLa/PMA
Competitor:
μ300
μ400
κE
SV40 E
κ pr.
1 2 3 4 5 6 7 8 9

FIGURE 25

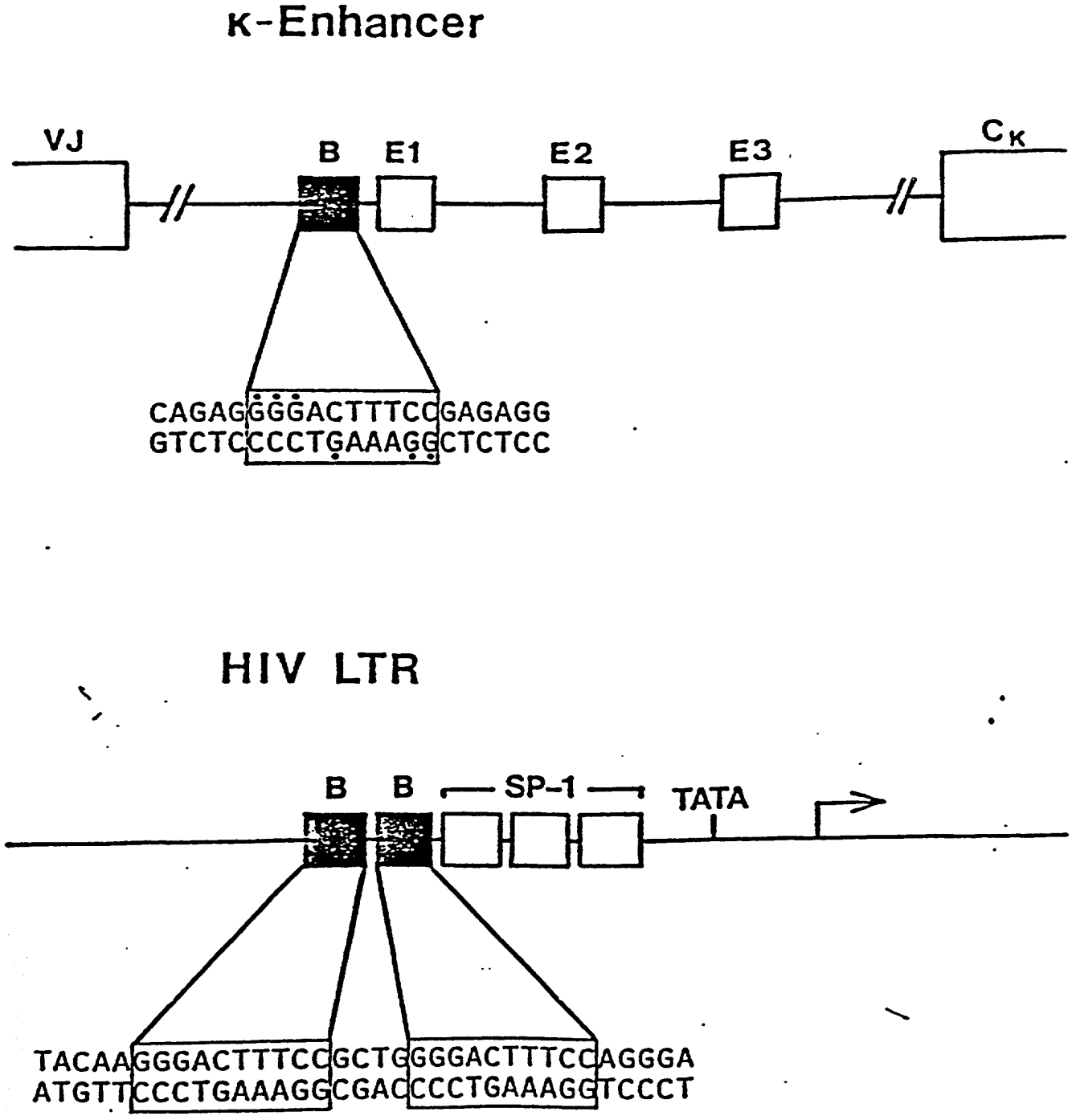

κ-Enhancer
VJ
B
E1
E2
E3
Cκ
CAGAGGGGACTTTCCGAGAGG
GTCTCCCCTGAAAGGCTCTCC
HIV LTR
B
B
SP-1
TATA
TACAAGGGACTTTCCGCTGGGGACTTTCCAGGGA
ATGTTCCCTGAAAGGCGACCCCTGAAAGGTCCCT

FIGURE 26

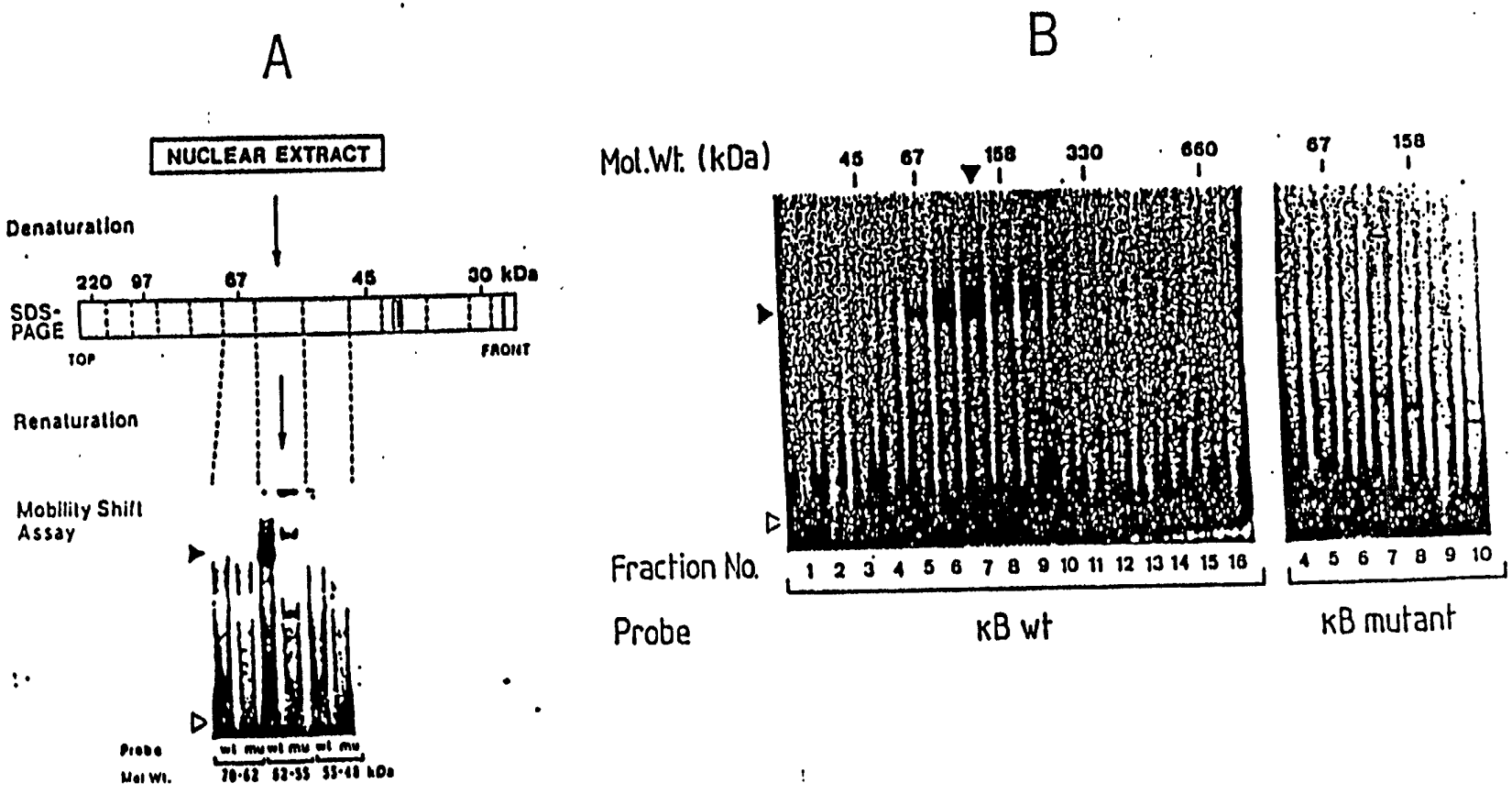


FIGURE 27

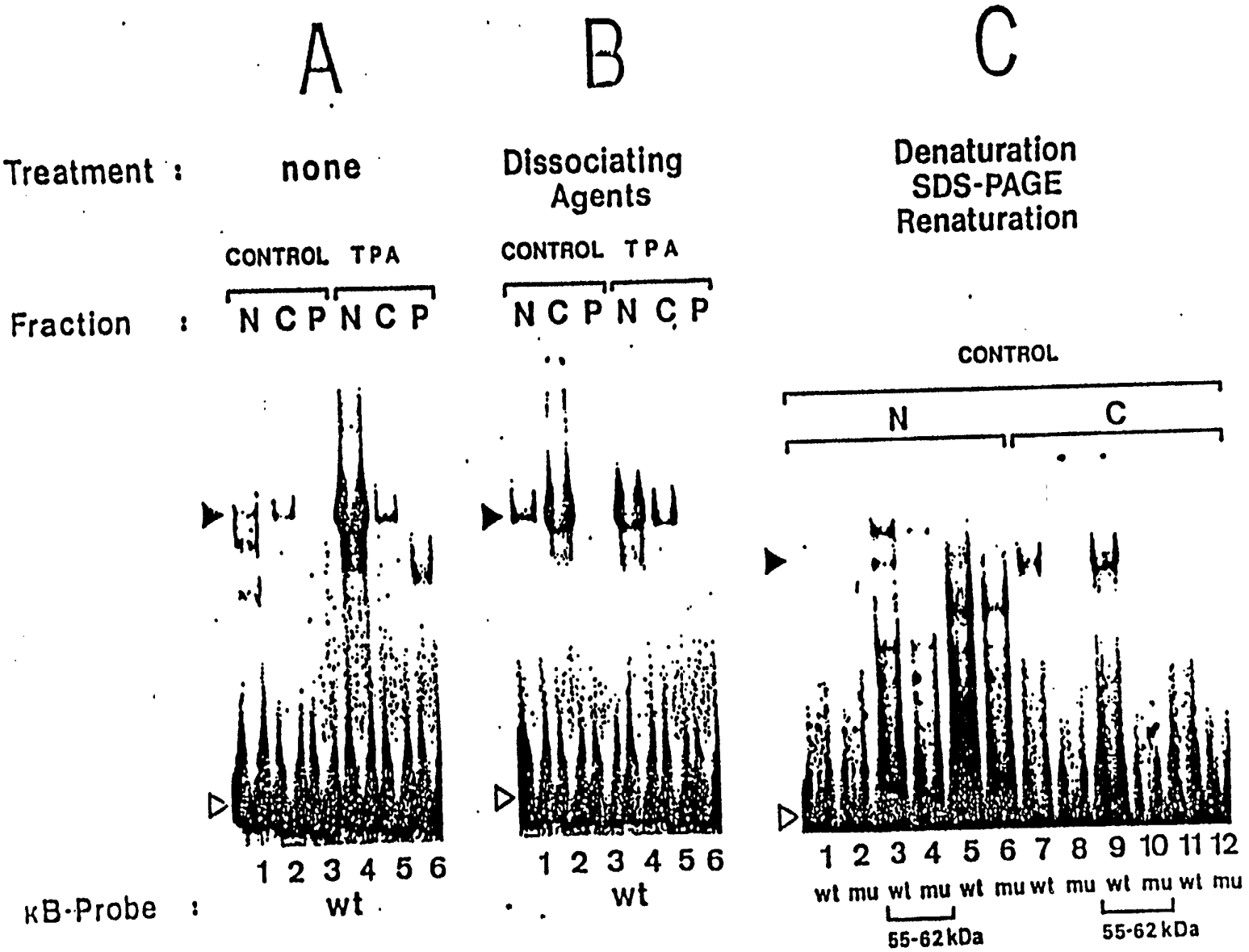

A
B
C
Treatment :
none
Dissociating Agents
Denaturation SDS-PAGE Renaturation
CONTROL TPA
CONTROL TPA
Fraction :
N C P N C P
N C P N C P
CONTROL
N
C
1 2 3 4 5 6
1 2 3 4 5 6
1 2 3 4 5 6 7 8 9 10 11 12
κB-Probe :
wt
wt
wt mu wt mu wt mu wt mu wt mu wt mu
55-62 kDa
55-62 kDa

FIGURE 28

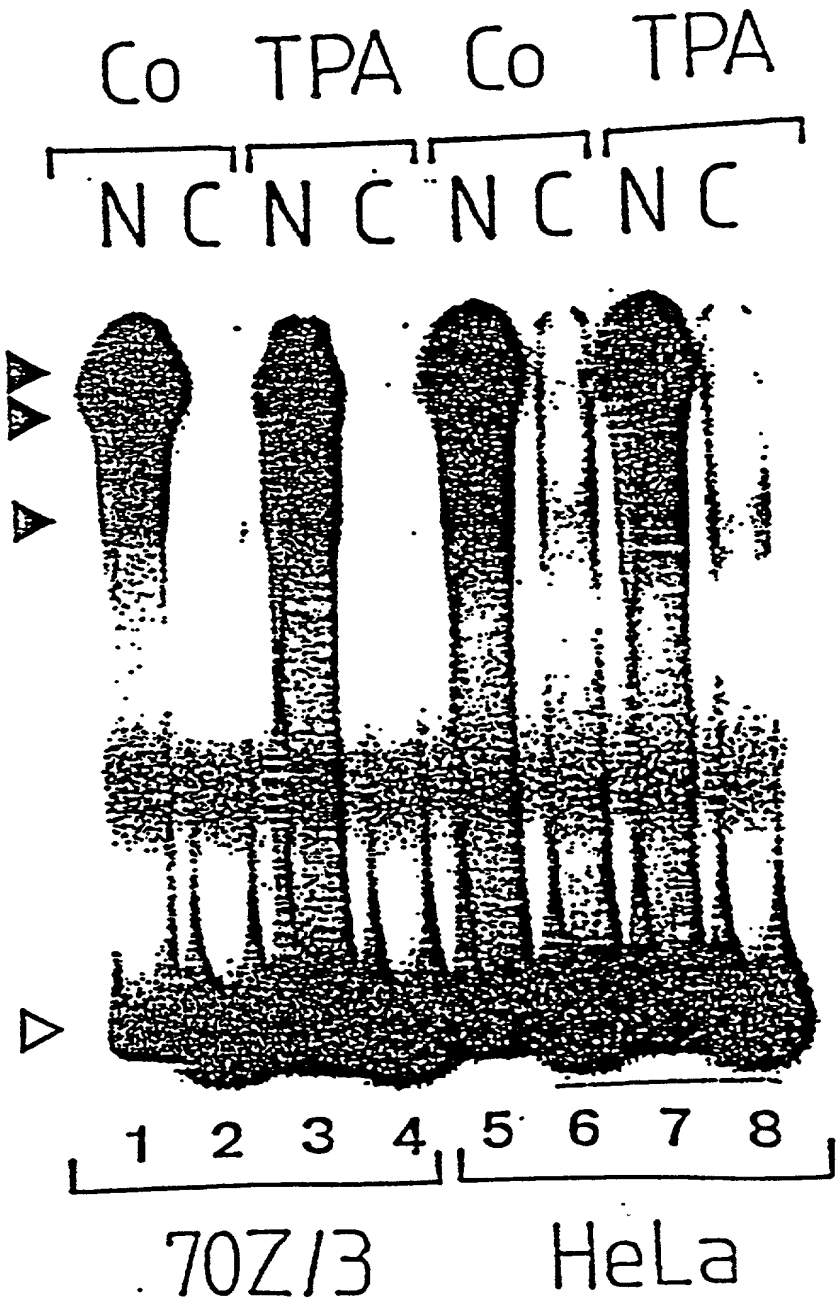


FIGURE 29

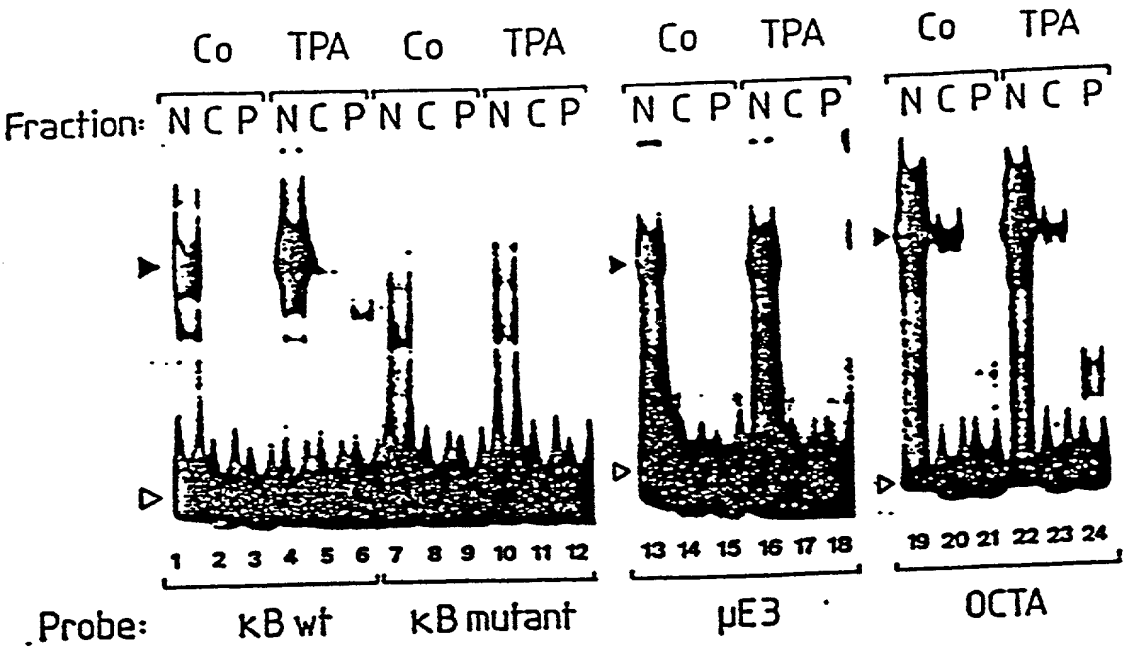


FIGURE 30

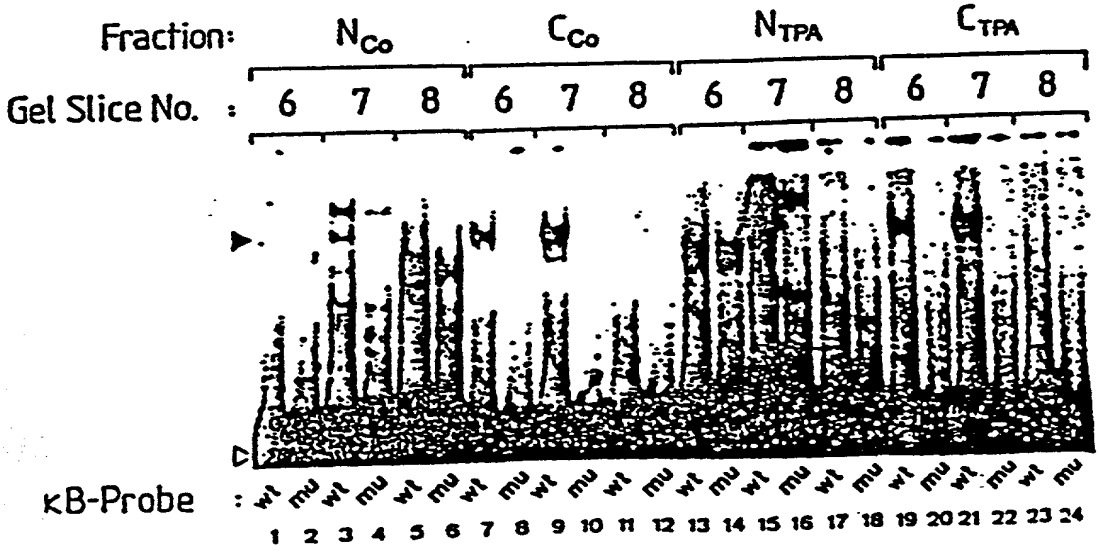


FIGURE 31

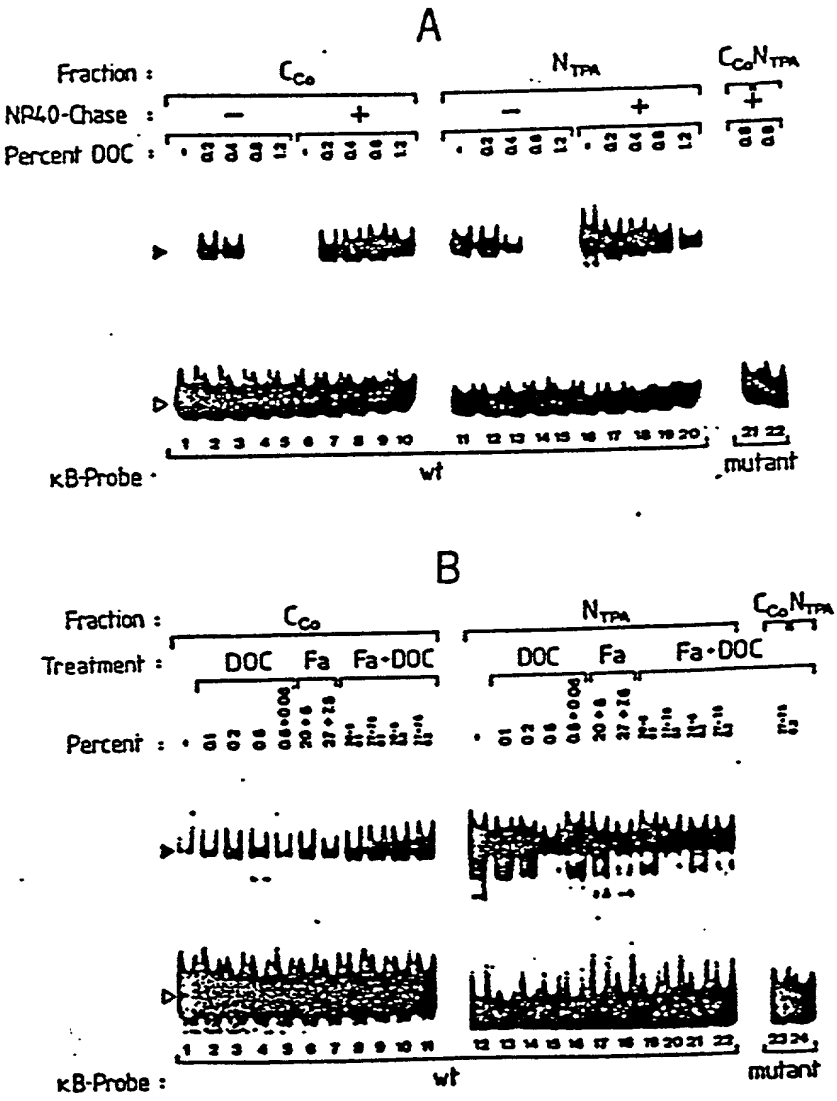

A
Fraction :
C_{Co}
N_{TPA}
$C_{Co}N_{TPA}$
NP40-Chase :
−
+
−
+
+
Percent DOC :
1 2 3 4 5 6 7 8 9 10
11 12 13 14 15 16 17 18 19 20
21 22
κB-Probe :
wt
mutant
B
Fraction :
C_{Co}
N_{TPA}
$C_{Co}N_{TPA}$
Treatment :
DOC
Fa
Fa+DOC
DOC
Fa
Fa+DOC
Percent :
1 2 3 4 5 6 7 8 9 10 11
12 13 14 15 16 17 18 19 20 21 22
23 24
κB-Probe :
wt
mutant

FIGURE 32

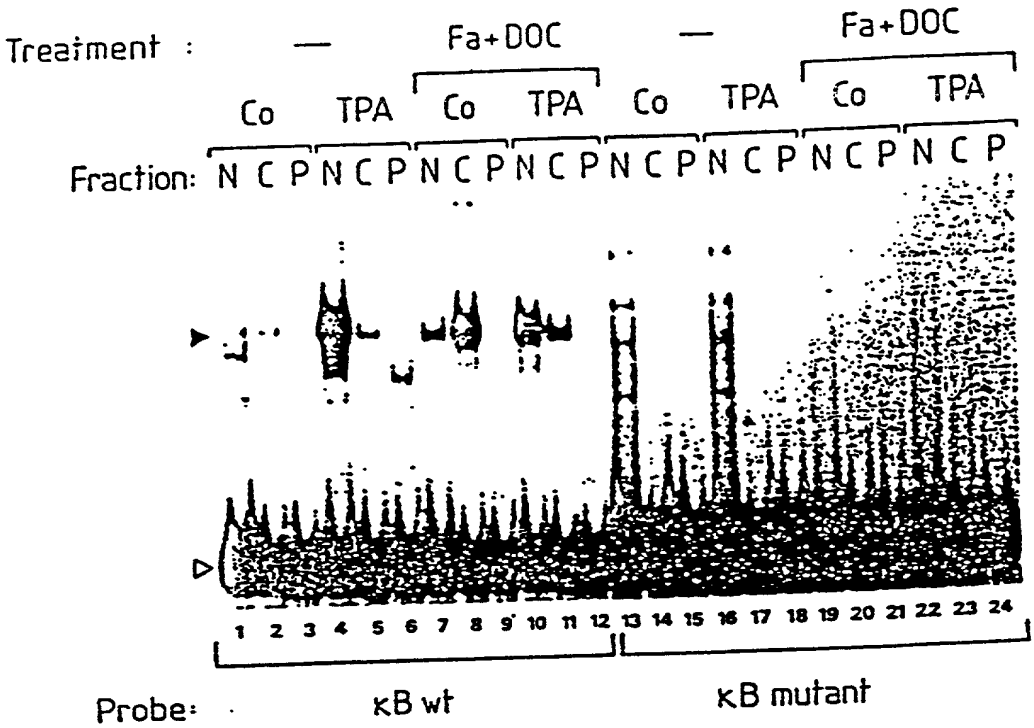


FIGURE 33

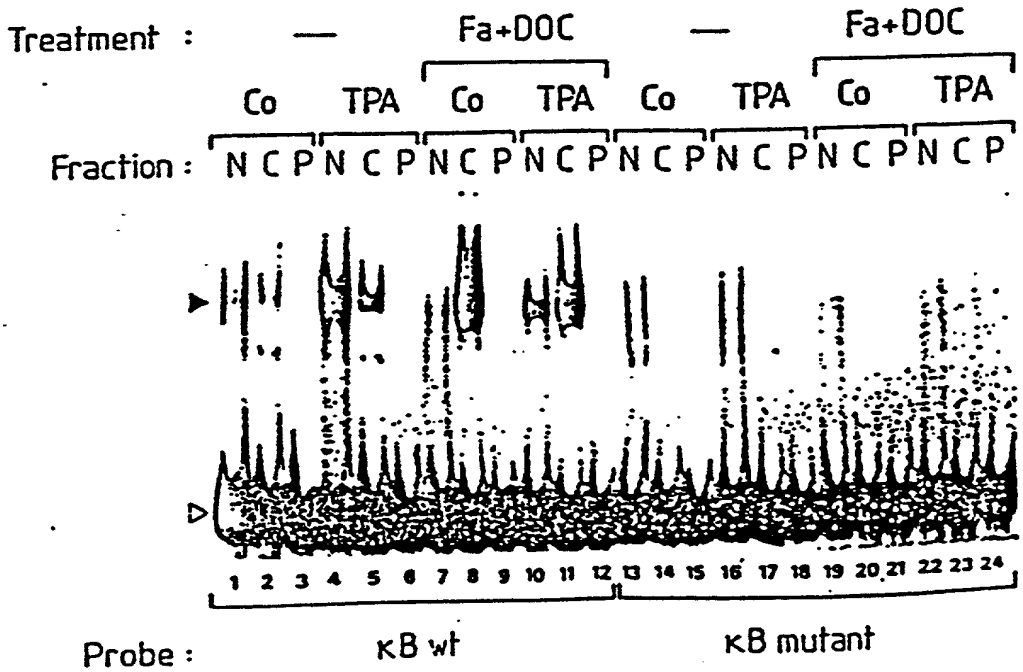


FIGURE 34

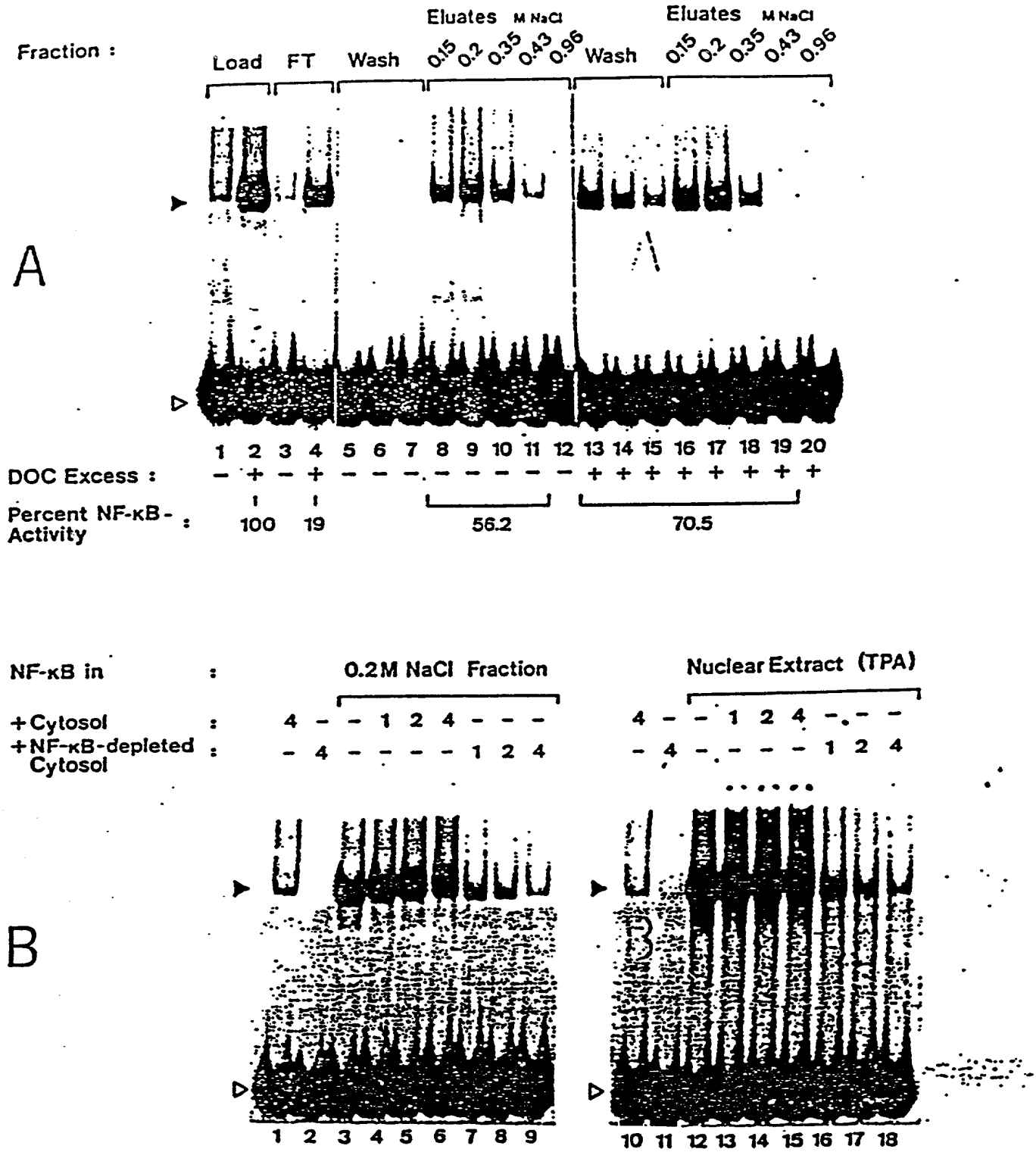

A
Fraction :
Load
FT
Wash
Eluates M NaCl
0.15
0.2
0.35
0.43
0.96
Wash
Eluates M NaCl
0.15
0.2
0.35
0.43
0.96
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
DOC Excess : – + – + – – – – – – – – + + + + + + + +
Percent NF-κB-Activity : 100 19 56.2 70.5
B
NF-κB in :
0.2M NaCl Fraction
Nuclear Extract (TPA)
+Cytosol : 4 – – 1 2 4 – – – 4 – – 1 2 4 – – –
+NF-κB-depleted Cytosol : – 4 – – – – 1 2 4 – 4 – – – – 1 2 4
1 2 3 4 5 6 7 8 9
10 11 12 13 14 15 16 17 18

FIGURE 35

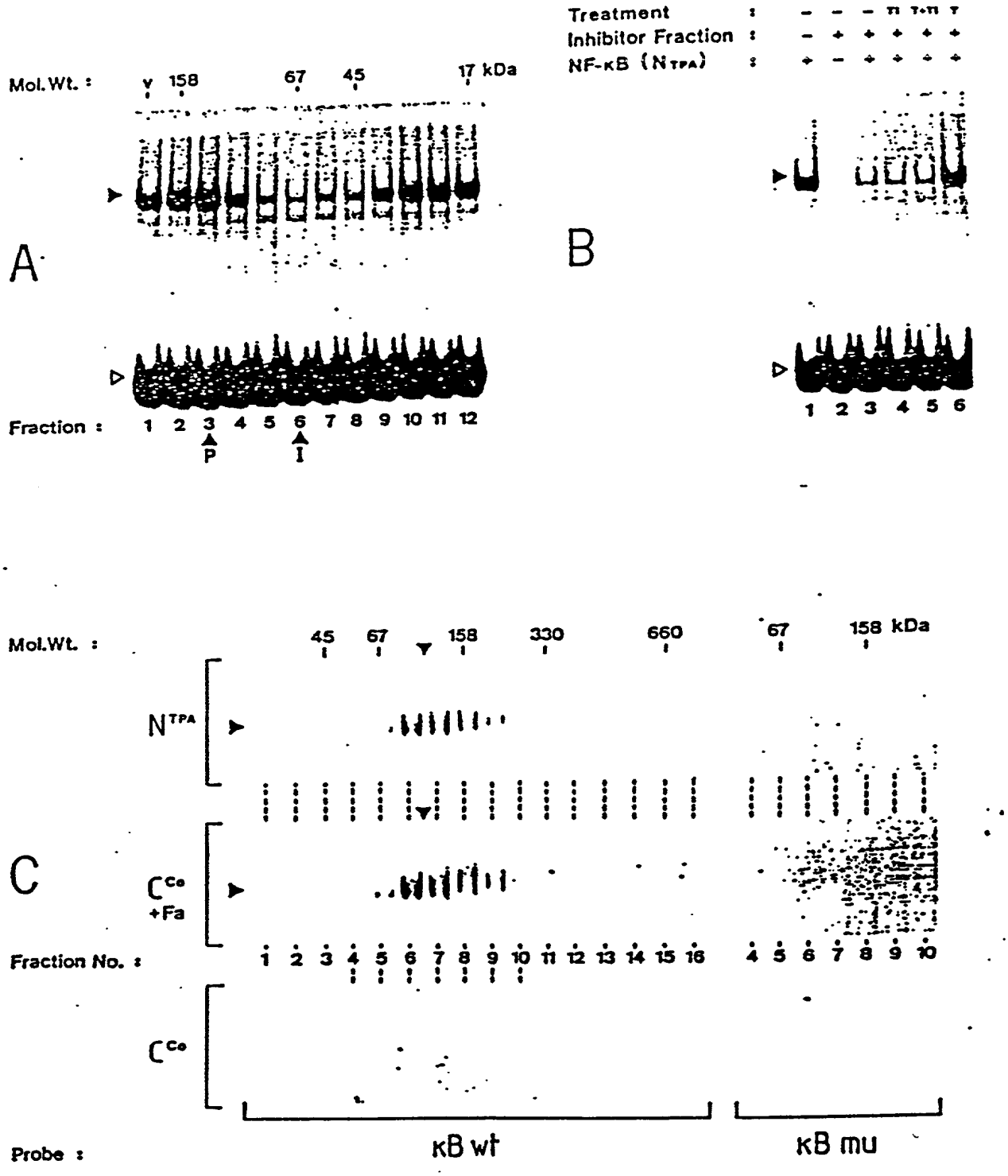

Mol.Wt. :
V 158 67 45 17 kDa
A
Fraction :
1 2 3 4 5 6 7 8 9 10 11 12
P
I
Treatment :
Inhibitor Fraction :
NF-κB (N TPA) :
B
1 2 3 4 5 6
Mol.Wt. :
45 67 158 330 660 67 158 kDa
N TPA
C
C Co +Fa
Fraction No. :
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 4 5 6 7 8 9 10
C Co
Probe :
κB wt
κB mu

FIGURE 36

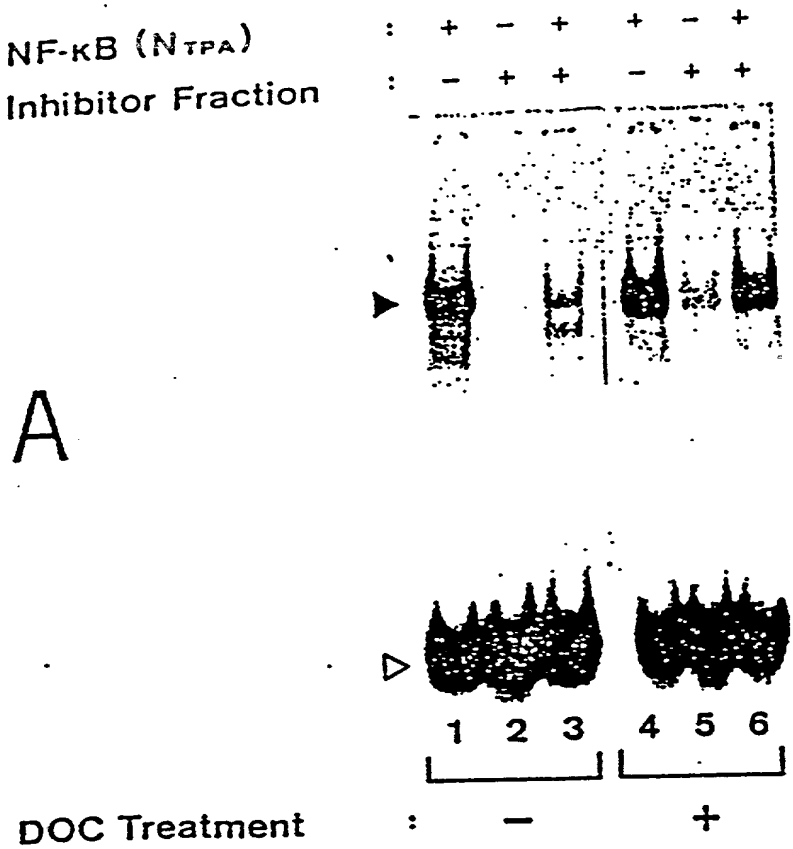
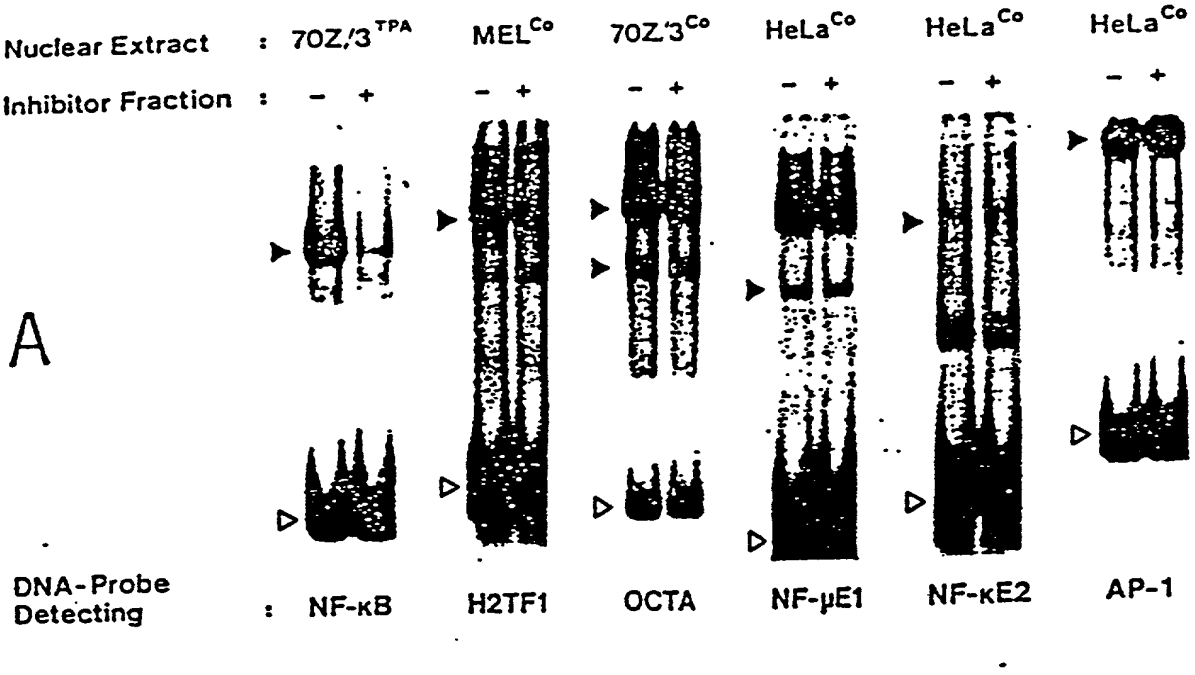

NF-κB (NTPA)
Inhibitor Fraction
: + − + + − +
: − + + − + +
A
1 2 3 4 5 6
DOC Treatment : − +
B
c.p.m. x 10-2
0
2
4
6
8
0
20
60 min
µl:
−
0.5
1.5
4.5

FIGURE 37


Nuclear Extract : 70Z/3TPA MELCo 70Z/3Co HeLaCo HeLaCo HeLaCo
Inhibitor Fraction : - + - + - + - + - + - +
A
DNA-Probe Detecting : NF-κB H2TF1 OCTA NF-μE1 NF-κE2 AP-1

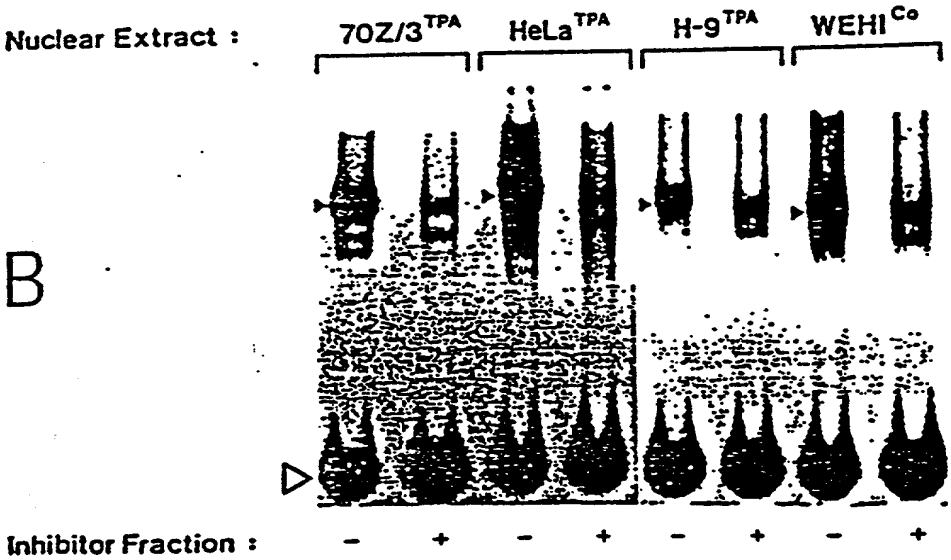
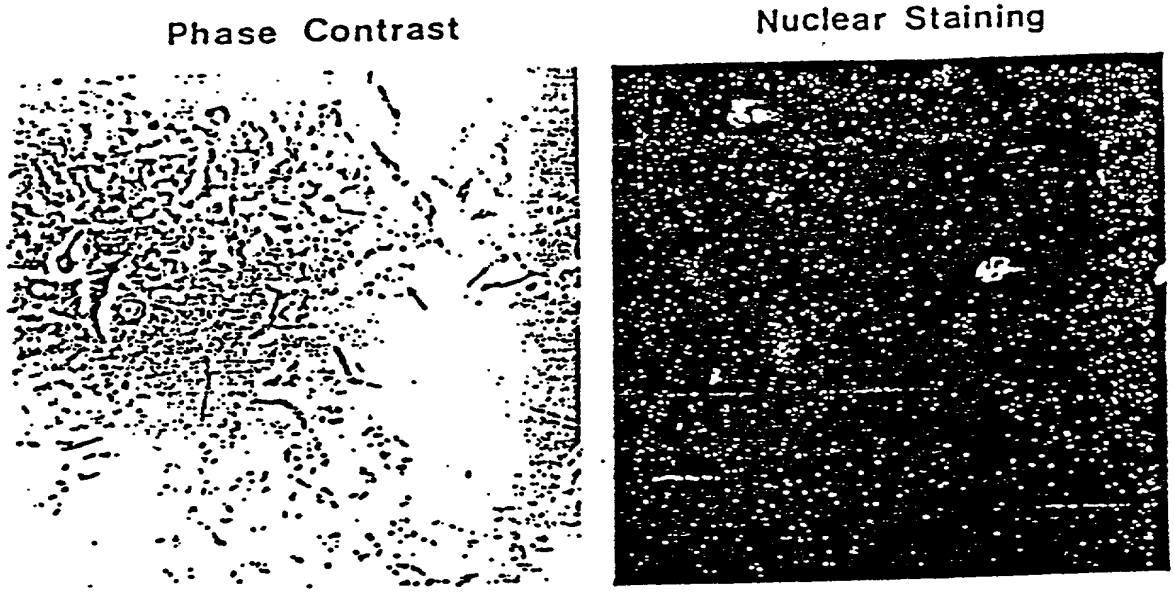

Nuclear Extract : 70Z/3TPA HeLaTPA H-9TPA WEHICo
B
Inhibitor Fraction : - + - + - + - +

FIGURE 38


Phase Contrast
Nuclear Staining
A
Enucleation : − + − + − +
Treatment of Cells : Co TPA Co TPA Co TPA Co TPA Co TPA Co TPA
B
1 2 3 4 5 6 7 8 9 10 11 12
Probe : κB κB AP-1
DOC-Treatment : − + −

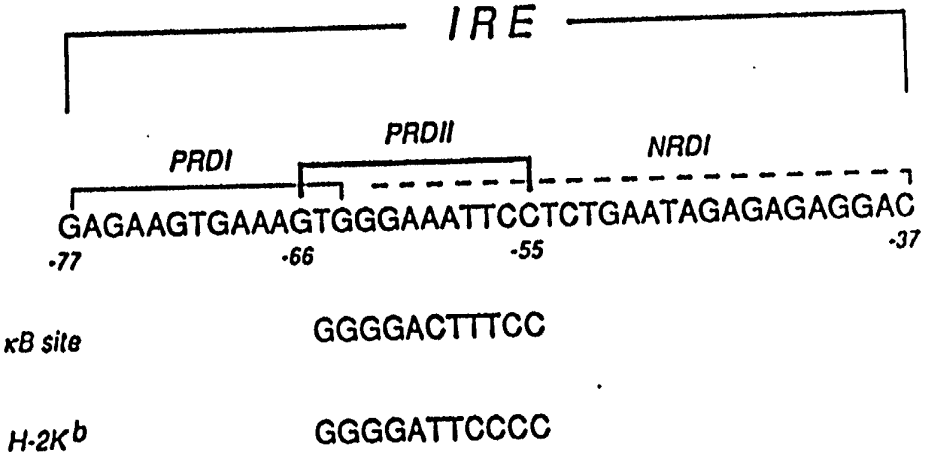

IRE
PRDI
PRDII
NRDI
GAGAAGTGAAAGTGGGAAATTCCTCTGAATAGAGAGAGGAC
-77
-66
-55
-37
κB site
GGGGACTTTCC
H-2Kb
GGGGATTCCCC

Figure 39

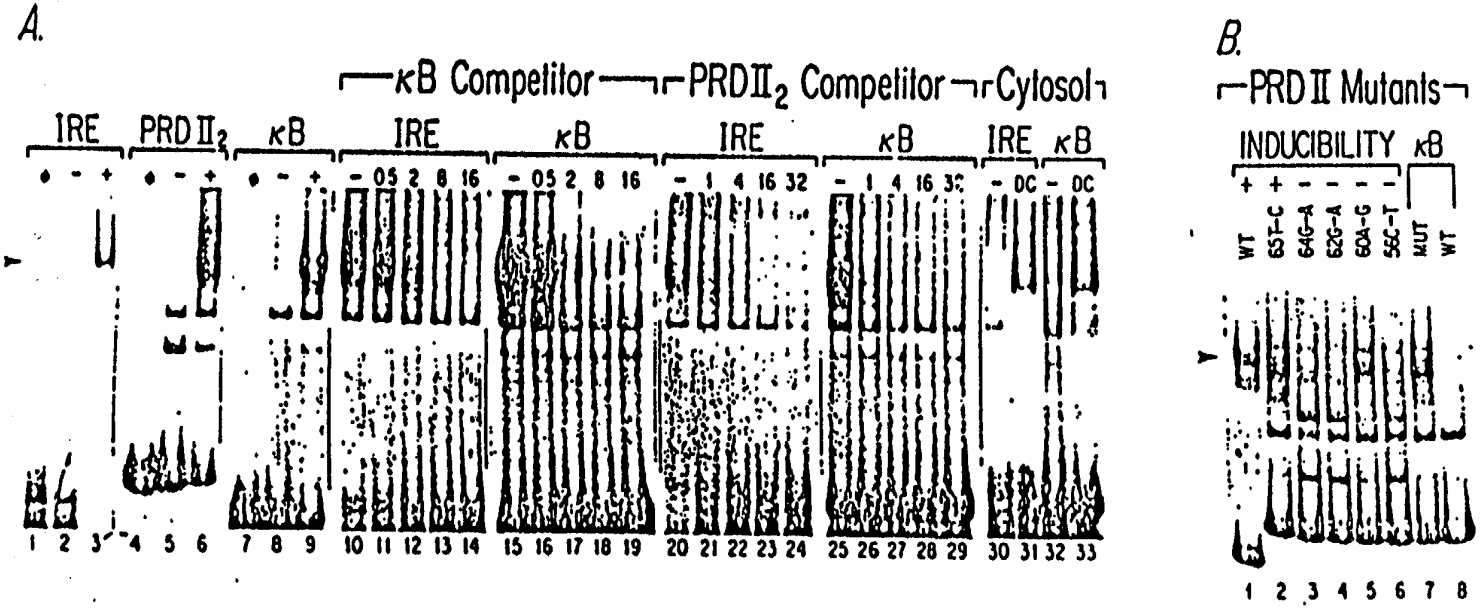


Figure 40

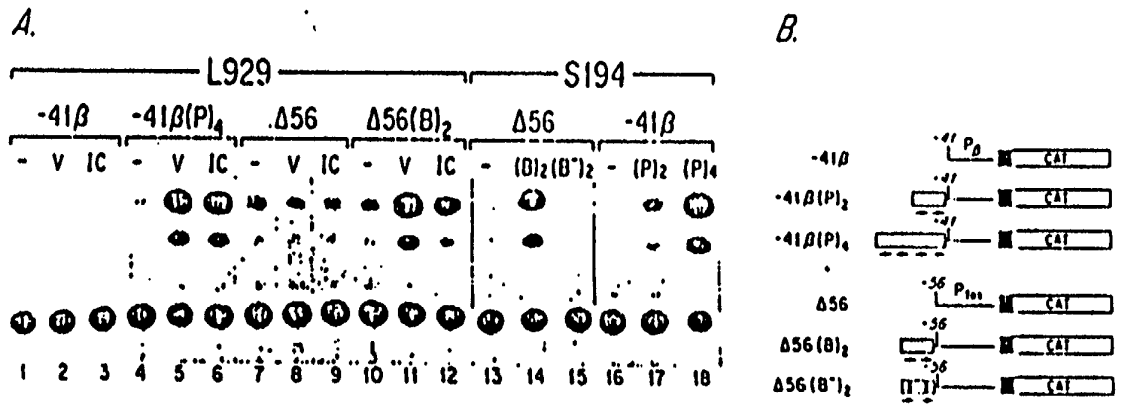

A.
L929
S194
-41β
-41β(P)4
Δ56
Δ56(B)2
Δ56
-41β
- V IC - V IC - V IC - V IC - (O)2(B⁻)2 - (P)2 (P)4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18
B.
-41β
-41β(P)2
-41β(P)4
Δ56
Δ56(B)2
Δ56(B⁻)2
CAT

Figure 41

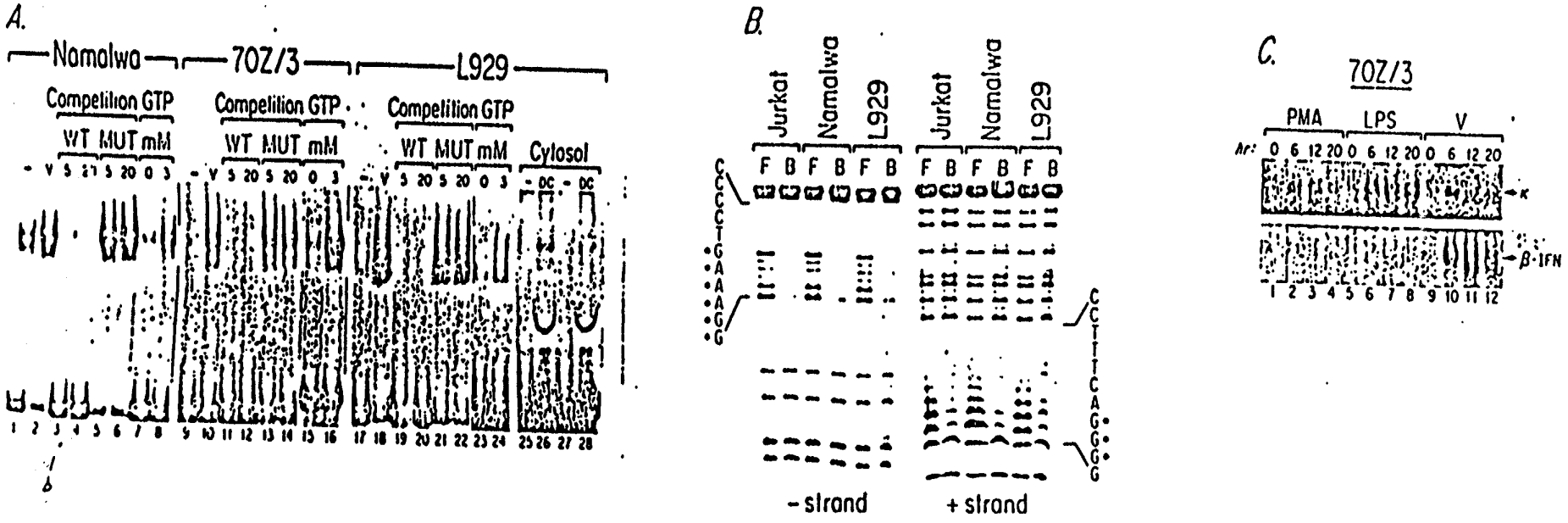


Figure 42

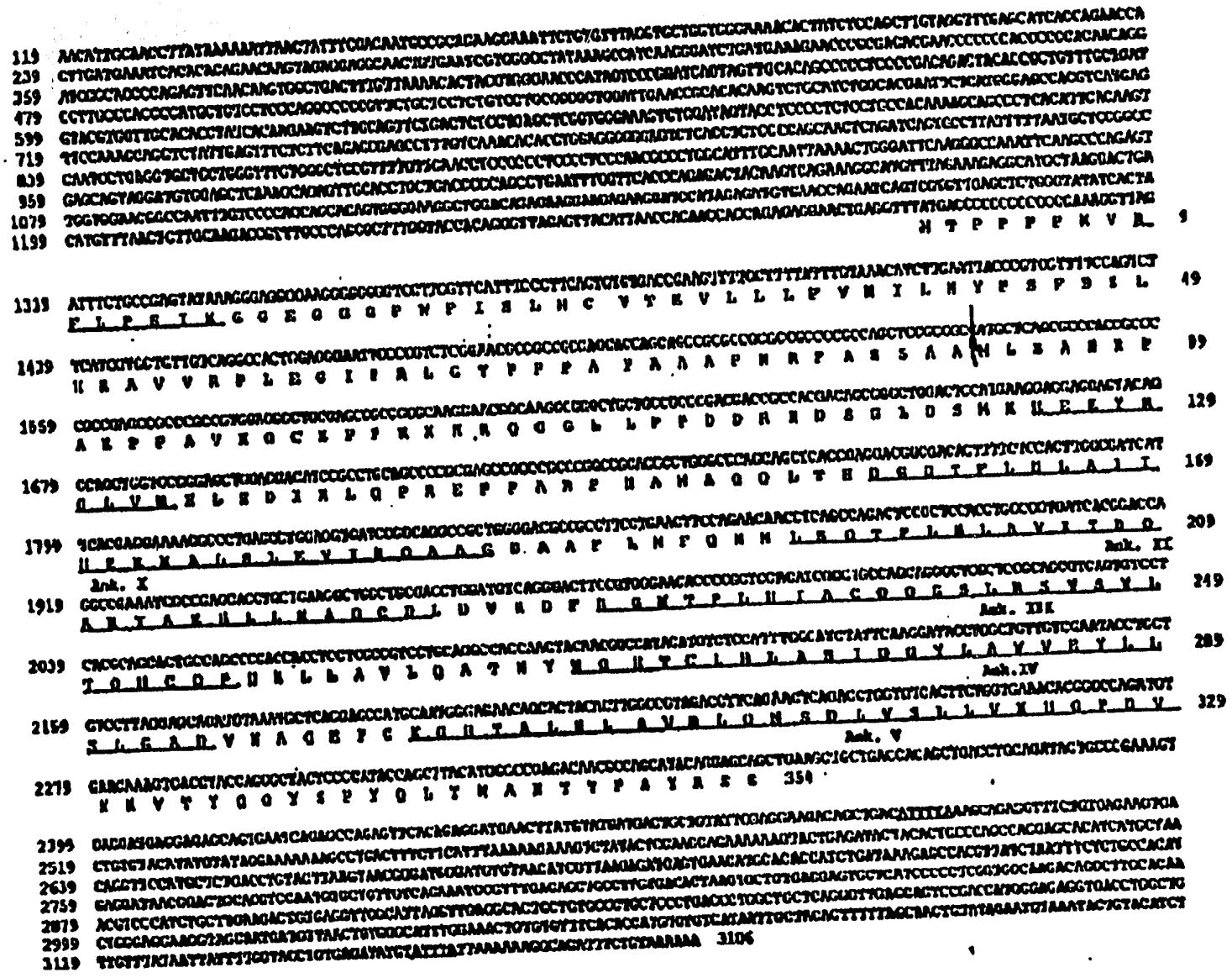


FIGURE 43